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                  19189..19378
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Best Local Similarity 99.5%; Pred. No. 3.8e-51;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 23862 CACACCAAGAGTGAAGCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTCT 23803
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DB 23802 TGGAGCCACAGACAGAGATTTGCTCTGTAAGGCTAAGCAGGTATCTCGTCACTGTG 23743
QY 181 GTCTTACCCCAAGCTGTGTA 201
DB 23742 GTCTTACCCCAAGCTGTGTA 23722

RESULT 2
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LOCUS           Homo sapiens chromosome 6 clone RP11-189014 map 6, LOW-PASS
DEFINITION      AC027197
SEQUENCE        AC027197.3 GI:9887745
ACCESSION       AC027197
VERSION         AC027197.3
KEYWORDS        HTG; HTGS-PHASED.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 194321)
Homo sapiens chromosome 6, clone RP11-189014
Unpublished
2 (bases 1 to 194321)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavsky, L., Bouckhagalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collins, R., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S.,
Dodgson, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D.,
Galagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, D. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
McCarthy, M., McKernan, P., McKernan, A., McKernan, K., McPheeters, R.,
Meldrum, J., Menus, L., Minova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Schauer, S., Severy, P.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-MAR-2006) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 194321)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,
Bouckhagalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choquet, Y., Colangelo, M., Collins, S., Collins, R., Cooke, P.,
DeArrellano, K., Dewar, K., Diaz, J. S., Dodgson, S., Ferreira, P.,
Fitzhugh, M., Gage, D., Galagan, J., Gardina, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Larocque, K.,
Lamazares, R., Lander, T., Lehoucq, Y., Levine, R., Lieu, C., Liu, G.,
Macdonald, P., Margulis, N., McCarthy, M., McKernan, P., McKernan, K.,
McPheeters, R., Meldrum, J., Menus, L., Minova, T., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, J., Oliver, J., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Schauer, S., Severy, P.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnuez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 24, 2000 this sequence version replaced gi:9799792.
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7625
Center clone name: 189_O_14

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* NOTE: This record contains 224 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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742
841: gap of 100 bp
842
1594: contig of 753 bp in length
1595
1694: gap of 100 bp
1695
2442: contig of 748 bp in length
2443
2542: gap of 100 bp
2543
3274: contig of 732 bp in length
3275
3374: gap of 100 bp
3375
4104: contig of 730 bp in length
4105
4204: gap of 100 bp
4205
4929: contig of 725 bp in length
4930
5029: gap of 100 bp
5030
5737: contig of 708 bp in length
5738
5837: gap of 100 bp
5838
6574: contig of 737 bp in length
6575
6674: gap of 100 bp
6676
7382: contig of 708 bp in length
7383
7482: gap of 100 bp
7483
8227: contig of 745 bp in length

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8228 8327: gap of 100 bp
8338 9072: contig of 745 bp in length
9073 9172: gap of 100 bp
9173 9920: contig of 748 bp in length
9921 10020: gap of 100 bp
10021 10740: contig of 720 bp in length
10741 10840: gap of 100 bp
10841 11566: contig of 726 bp in length
11567 12407: contig of 741 bp in length
12408 12507: gap of 100 bp
12508 13254: contig of 747 bp in length
13255 13354: gap of 100 bp
13355 14095: contig of 741 bp in length
14096 14195: gap of 100 bp
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16585 17433: contig of 749 bp in length
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43231 43953: contig of 733 bp in length
43954 44063: gap of 100 bp
44064 44771: contig of 708 bp in length
44772 44871: gap of 100 bp
44872 45584: contig of 713 bp in length
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Best Local Similarity 99.5%; Pred. No. 3.7e-51;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGACATCCTCATCTTTTCTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 60
Db 10570 TTGACATCCTCATCTTTTCTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 10511
QY 61 CACACCAAGAGGAACTCGAATCATGTTGAGAAATGAAAGTGTAGGCTGTTCT 120
Db 10510 CACACCAAGAGGAACTCGAATCATGTTGAGAAATGAAAGTGTAGGCTGTTCT 10451
QY 121 TGGAGCCCAACAGAGCATATTCCTTCTAAGCTAAGCAAGTACTGGCTACCTGTG 180
Db 10450 TGGAGCCCAACAGAGCATATTCCTTCTAAGCTAAGCAAGTACTGGCTACCTGTG 10391
QY 181 GTCTTCACTCCCAAGCTGTGCA 201
Db 10390 GTCTTCACTCCCAAGCTGTGCA 10370

RESULT 3
LOCUS HUMPLG20 331 bp DNA linear PRI 07-JAN-1995
DEFINITION Human plasminogen gene, exon 16.
ACCESSION M34272 J05286
VERSION M34272.1 GI:190060
KEYWORDS plasminogen.
SEGMENT 20 of 24
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 331)
AUTHORS Petersen,T.E., Mattzen,M.R., Ichinose,A. and Davie,E.W.
TITLE Characterization of the gene for human plasminogen, a key proenzyme
in the fibrinolytic system
J. Biol. Chem. 265 (11), 6104-6111 (1990)
JOURNAL PUBMED 2318848
COMMENT Original source text: Homo sapiens DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by A. Ichinose, 26-MAR-1990, for release after publication.
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Intron

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Intron

ORIGIN      Undetermined number of base pairs after segment 19.

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Best Local Similarity 95.5%; Pred. No. 4,6e-47;
Matches 192; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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Db      19 TTGACATCCTCATCTTTTCTAGGTCTCAAGGCTTCATCTACAGGTATCTGGGTG 78

QY      61 CACACCAAGAGTGAAGTCTGAATCTCATGTTCAGAAATGAGAGTGTAGGCTTCT 120
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QY      121 TGGAGCCACACAGAGATATTTGCTTGTCTAAGCTAAGCAGAGTACTGCTCAGCTGTG 180
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Db      139 TGGAGCCACACAGAGATATTTGCTTGTCTAAGCTAAGCAGAGTACTGCTCAGCTGTG 198

QY      181 GTCTTCACCCGACGCTGTGA 201
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LOCUS      Homo sapiens plasminogen (PLG) gene, complete cds.
DEFINITION      AY192161
ACCESSION      AY192161
VERSION      AY192161.1 GI:27228744
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 55266)
Rieder,M.J., Armet,T.Z., Carrington,D.P., Ozuna,M., Kulane,K.S.A.,
Rajkumar,N., Torch,E.J., Yi,Q. and Nickerson,D.A.
Direct Submission
Submitted (07-DEC-2002) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: SeattleSNP, NHLBI HL66682 Program
for Genomic Applications, UW-FHRC, Seattle, WA (URL:
http://pga.gs.washington.edu).
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KGTGENTRGVAVTVSGTCDHMSAOTPHNRPENPCKNDLNTCRNPDGRAM
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LKKGSGTEASVAPRPVLLPDVETPSEEDCMFNGKYGKALTYTTPCODMAWQ
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EKSPRESYKIVGIAHQBVLDPHVOETIEVSRLEFETRDIALIKSSPAVTTDKYI
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Best Local Similarity 95.5%; Pred. No. 3.7e-47;
Matches 192; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 1 TTGACATCTCATCTTTCTAGGTCCTCAAGCCTTCATCTCAAGGTCATCTCGGATG 60
Db 39282 TTGACATCTCATCTTTCTAGGTCCTCAAGCCTTCATCTCAAGGTCATCTCGGATG 39341
QY 61 CACACCAAGAGTGAACCTCGAATCTCATGTCAGAAATGAAAGTCTTAGGCTGTCT 120
Db 39342 CACACCAAGAGTGAACCTCGAATCTCATGTCAGAAATGAAAGTCTTAGGCTGTCT 39401
QY 121 TGAAGCCACACACAGAGATATGCTTGTGAAGTGAAGCAGTCTCGCTCAACCTGTG 180
Db 39402 TGAAGCCACACACAGAGATATGCTTGTGAAGTGAAGCAGTCTCGCTCAACCTGTG 39461
QY 181 GTCTTCAACCCACGCTGTGA 201
Db 39462 GTCTTCAACCCACGCTGTGA 39482
RESULT 5
HSDJ81D8 163599 bp DNA linear PRI 18-MAY-2005
LOCUS Human DNA sequence from clone RPI-81D8 on chromosome 6q25.3-26
DEFINITION Contains the PLG gene for plasminogen, the 5' end of the LPA gene
for lipoprotein (Lp(a)), a novel gene, a pseudogene similar to part
of plasminogen and a CpG island, complete sequence.
ACCESSION AL109933 GI:11344445
VERSION 1
KEYWORDS HTG; apolipoprotein; Cpg; kringie; lipoprotein; LPA; plasminogen;
PLG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 163599)
REFERENCE
1 Tracey, A.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Nov 25, 2000 this sequence version replaced gi:11322966.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrt
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
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Web site: <http://www.sanger.ac.uk>
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
RPI-81d8 is from the library RPCI-1 constructed by the group of Pletier de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

Location/Qualifiers

1. 16359

/organism="Homo sapiens"

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/clone="RPI-81d8"

/clone_1fb="RPCI-1"

1

/note="Clone left end: RPI-81d8"

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complement(AL596089.19:15200..130112))

/gene="LPA"

/locus_tag="RPI1-414A5.1-001"

join(complement(14132..14225), complement(304..463),

complement(AL596089.19:129931..130112),

complement(AL596089.19:128564..128723),

complement(AL596089.19:124384..124565),

complement(AL596089.19:123017..123176),

complement(AL596089.19:118840..119021),

complement(AL596089.19:117470..117629),

complement(AL596089.19:113291..113472),

complement(AL596089.19:111974..112081),

complement(AL596089.19:107727..107928),

complement(AL596089.19:106380..106539),

complement(AL596089.19:102201..102382),

complement(AL596089.19:100834..100993),

complement(AL596089.19:96649..96830),

complement(AL596089.19:95279..95438),

complement(AL596089.19:90194..90375),

complement(AL596089.19:88763..88922),

complement(AL596089.19:84634..84815),

complement(AL596089.19:83217..83376),

complement(AL596089.19:79071..79252),

complement(AL596089.19:77675..77834),

complement(AL596089.19:74661..74818),

complement(AL596089.19:73270..73429),

complement(AL596089.19:70166..70347),

complement(AL596089.19:68763..68922),

complement(AL596089.19:62240..62421),

complement(AL596089.19:60853..61012),

complement(AL596089.19:41107..41288),

complement(AL596089.19:39742..39901),

complement(AL596089.19:32195..32376),

complement(AL596089.19:31506..31654),

complement(AL596089.19:29157..29250),

complement(AL596089.19:26405..26555),

complement(AL596089.19:24824..24988),

complement(AL596089.19:23760..23900),

complement(AL596089.19:21572..21678),

complement(AL596089.19:16248..16366),

complement(AL596089.19:15200..15607))

/gene="LPA"

/locus_tag="RPI1-414A5.1-001"

/note="match: ESTs: BF970104.1

match: cDNA: X06290.1"

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CDS

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complement(AL596089.19:128564..128723),
complement(AL596089.19:124384..124565),
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complement(AL596089.19:113291..113472),
complement(AL596089.19:111974..112081),
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complement(AL596089.19:102201..102382),
complement(AL596089.19:100834..100993),
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complement(AL596089.19:95279..95438),
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complement(AL596089.19:84634..84815),
complement(AL596089.19:83217..83376),
complement(AL596089.19:79071..79252),
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complement(AL596089.19:73270..73429),
complement(AL596089.19:70166..70347),
complement(AL596089.19:68763..68922),
complement(AL596089.19:62240..62421),
complement(AL596089.19:60853..61012),
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complement(AL596089.19:41107..41288),
complement(AL596089.19:39742..39901),
complement(AL596089.19:32195..32376),
complement(AL596089.19:31506..31654),
complement(AL596089.19:29157..29250),
complement(AL596089.19:26405..26555),
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complement(AL596089.19:23760..23900),
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/locus_tag="RPI1-414A5.1-001"
/standard_name="OTRHMP0000017543"
/note="match: proteins: P08519"
/codon_start=2
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/db_xref="GI:56203915"
/db_xref="GOA:Q5VTD7"
/db_xref="InterPro:IPR000001"
/db_xref="InterPro:IPR001254"
/db_xref="InterPro:IPR001314"
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/translation="MEHKEVLLLLFLKSAAPQSHVODCHGDGOSYGTSTTV
TGRTCQAMSSMTPHQNRRTTENYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNL
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RTOCAMSSMTPHSHSTRPEYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNLTO
CSDAAGTAAPPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
QOAMSSMTPHSHSTRPEYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNLTOCS
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DAAGTAAPPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
EGTAAPPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
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TAAPPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
MTPHSHSTRPEYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNLTOCS
VAPPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
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PPTVTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
SHSTRPEYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNLTOCS
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SRTAAYTPVPSLEAPSEQAFTPEORPGVOCYHNGOSYRGTSTTVGRT
ILASLEAFEPQALTEETPGVODCYTHGDSYRGTSTTVGRT
TPENYVNAQIMNYCRNPDAVAAPCYTRDPGRVMEYCNLTOCS
DPTSEASEAPTEOSPGVODCYHNGOSYRGTSTTVGRT
EYVNGGLTRYVNCNPDAEISPMCYTMDPVNRYMEYCNLTOCS
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/locus_tag="Rpl-81D8.4-001"
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/note="match: proteins: 018783 046507 P00747 P06867 P06868 P12345 P20918 P80009 P80010 P81286 Q15146 Q29485 Q91WU5 Q9R0W3"
/pseudo

CDS
complement(join(16194..16339,26376..26489))
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Query Match 92.8% Score 186.2; DB 5; Length 16359;
Best Local Similarity 95.0%; Pred. No. 1.1e-46;
Matches 191; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TTGACATCCTCATCTTTCTAGTCTCTAGAGCCTTCTACAGGCTCATCTGGGTG 60
Db 89012 TTGACGCTCTCATCTTTCTAGTCTCTAGAGCCTTCTACAGGCTCATCTGGGTG 89071

Qy 61 CACACCAAGAGTGAAGCTGCAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCT 120
Db 89072 CACACCAAGAGTGAATCTGCAACCGCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCT 89131

Qy 121 TGGAGCCCAACAGCAATATGCTGCTTAAAGCTAAGAGGACTCGCTACCGCTG 180
Db 89132 TGGAGCCCAACAGCAATATGCTGCTTAAAGCTAAGAGGACTCGCTACCGCTG 89191

Qy 181 GTCTTACACCCACCGCTGCTGA 201
Db 89192 GTCTTACACCCACCGCTGCTGA 89212

RESULT 6
AC010893/c 177878 bp DNA 1linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 6 clone RP11-480A20, WORKING DRAFT
DEFINITION
SEQUENCE, 18 unordered pieces.
AC010893
AC010893.5 GI:8568869
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 177878)
Materston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 177878)
Materston, R.H.
Direct Submission
Submitted (25-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108 USA
On Jun 16, 2000 this sequence version replaced gi:6850583.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: MUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----

Center project name: H_NH0480A20
----- Summary Statistics -----
Sequencing vector: M13; 76%
Sequencing vector: plasmid; 24%
Chemistry: Dye-terminator ET; 76% of reads
Chemistry: Dye-terminator Big Dye; 24% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165387 bases at least Q40
Consensus quality: 170279 bases at least Q30
Consensus quality: 172646 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 176178; sum-of-contigs
Quality coverage: 4.11 in Q20 bases; sum-of-contigs
Quality coverage: 4.01 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 1046: contig of 1046 bp in length
1047 1146: gap of unknown length
1147 2235: contig of 1089 bp in length
2236 2335: gap of unknown length
2336 3349: contig of 1014 bp in length
3350 3449: gap of unknown length
3450 5172: contig of 1723 bp in length
5173 5272: gap of unknown length
5273 7349: contig of 2077 bp in length
7350 7449: gap of unknown length
7450 9861: contig of 2412 bp in length
9862 9961: gap of unknown length
9962 13599: contig of 3638 bp in length
13600 13699: gap of unknown length
13700 16835: contig of 3136 bp in length
16836 16935: gap of unknown length
16936 21649: contig of 4714 bp in length
21650 21749: gap of unknown length
21750 28521: contig of 6772 bp in length
28522 28621: gap of unknown length
28622 36536: contig of 7935 bp in length
36537 36556: gap of unknown length
36557 45767: contig of 9111 bp in length
45768 45867: gap of unknown length
45868 59019: contig of 13152 bp in length
59020 59119: gap of unknown length
59120 75610: contig of 16491 bp in length
75611 75710: gap of unknown length
75711 93797: contig of 18087 bp in length
93798 93897: gap of unknown length
93898 116372: contig of 22475 bp in length
116373 116472: gap of unknown length
116473 144933: contig of 28461 bp in length
144934 145033: gap of unknown length
145034 177878: contig of 32845 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-480A20"
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1047..1146
/estimated_length=unknown
1147..2235
/note="assembly_name:Contig41"
2236..2335
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gap 5173..5272
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gap 9862..9961
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misc_feature 9962..13599
/contig="assembly_name:Contig56"
gap 13600..13699
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misc_feature 13700..16835
/contig="assembly_name:Contig57"
gap 16836..16935
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gap 21650..21749
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gap 75611..75710
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ORIGIN

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Query Match 92.8%; Score 186.2; DB 12; Length 177878;
Best Local Similarity 95.0%; Pred. No. 1,1e-46;
Matches 191; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
1 TTGACATCTCATCTTTTCTAGTCTCTGAGGCTTCACTCTACAAAGTCACTCTGGGTG 60
Db 171500 TTGACATCTCATCTTTTCTAGTCTCTGAGGCTTCACTCTACAAAGTCACTCTGGGTG 171441

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QY 61 CACACCAAGAAGTGAACCTCGAATCTCATGTTTCAGGAAATRGAGTCTAGCTGTCT 120
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QY 121 TGGAGCCCAACAGACAGATATTGCTTCTTAAGTAAAGTACAGATCTGGCTACCTGTG 180
DB 171380 TGGAGCCCAACAGAAAGATATTGCTTCTTAAGTAAAGCAGATCTGTTACCTGTG 171321
QY 181 GTCTTCACCCAACGCTGTGA 201
DB 171320 GTCTTCACCCAACGCTGTGA 171300

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RESULT 7

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AC084862/c 179154 bp DNA linear HTG 26-JUL-2005
LOCUS Papio anubis clone rp41-286p17, WORKING DRAFT SEQUENCE, 2 ordered
DEFINITION

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ACCESSION AC084862
VERSION AC084862.14 GI:59797159
HTG: HTGS PHASE2; HTGS DRAFT.
KEYWORDS
SOURCE Papio anubis (olive baboon)
ORGANISM

```

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REFERENCE
AUTHORS Lau,C., Boffelli,D. and Roe,B.A.
TITLE Papio anubis BAC Clone rp41-286p17
JOURNAL Unpublished
REFERENCE
AUTHORS Lau,C., Boffelli,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

```

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REFERENCE
AUTHORS Lau,C., Boffelli,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2005) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT
On Feb 15, 2005 this sequence version replaced gi:55701371.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 68162 contig of 68161 bp in length
* 68162 gap of unknown length
* 68262 179154: contig of 110893 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9555"
/clone="rp41-286p17"
/clone_lib="RPCI - 41 Male (Olive) Baboon BAC Library"
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FEATURES

source

ORIGIN

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Query Match 86.7%; Score 174; DB 12; Length 179154;

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TITLE
JOURNAL
COMMENT

Lamazares, R., Landers, T., Lechoczky, J., Levine, R., Lieu, C., Liu, G.,
McDonald, P., Margulis, N., McCarthy, M., McEwan, P., McKernan, K.,
McPherson, R., Melgrim, J., Meneses, L., Mihova, T., Mlenga, V.,
Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Oliver, J., Oliver, J., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Ribback, M., Riley, R.,
Rogov, P., Rochman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sousnez, C., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Strassman, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Travers, M., Triggilio, J., Vassiliou, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zimmer, A., and Zody, M.

Submitted (24-ANG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 24, 2000 this sequence version replaced gi:9799792.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7625

Center clone name: 189_O_14

* NOTE: This record contains 224 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 741: contig of 741 bp in length

742 841: gap of 100 bp

842 1594: contig of 753 bp in length

1595 1694: gap of 100 bp

1696 2442: contig of 748 bp in length

2443 2542: gap of 100 bp

2543 3274: contig of 732 bp in length

3275 3375: gap of 100 bp

3376 4104: contig of 730 bp in length

4105 4204: gap of 100 bp

4206 4929: contig of 725 bp in length

4930 5029: gap of 100 bp

5030 5737: contig of 708 bp in length

5738 5837: gap of 100 bp

5838 6574: contig of 737 bp in length

6575 6674: gap of 100 bp

6676 7382: contig of 708 bp in length

7383 7482: gap of 100 bp

7483 8227: contig of 745 bp in length

8228 8327: gap of 100 bp

8329 9072: contig of 745 bp in length

9073 9172: gap of 100 bp

9173 9920: contig of 748 bp in length

9921 10020: gap of 100 bp

10021 10740: contig of 720 bp in length

10741 10840: gap of 100 bp

10841 11566: contig of 726 bp in length

11567 11667: gap of 100 bp

11668 12407: contig of 741 bp in length

12408 12507: gap of 100 bp

12508 13254: contig of 747 bp in length

13255 13354: gap of 100 bp

13355 14095: contig of 741 bp in length

14096 14195: gap of 100 bp

14196 14933: contig of 738 bp in length
14934 15033: gap of 100 bp
15034 15755: contig of 722 bp in length
15756 15855: gap of 100 bp
15856 16584: contig of 729 bp in length
16585 16684: gap of 100 bp
16685 17433: contig of 749 bp in length
17434 17533: gap of 100 bp
17534 18286: contig of 753 bp in length
18287 18387: gap of 100 bp
18388 19127: contig of 741 bp in length
19128 19227: gap of 100 bp
19228 19937: contig of 710 bp in length
19938 20037: gap of 100 bp
20038 20750: contig of 713 bp in length
20751 20850: gap of 100 bp
20851 21574: contig of 724 bp in length
21575 21674: gap of 100 bp
21675 22395: contig of 721 bp in length
22396 22495: gap of 100 bp
22496 23225: contig of 730 bp in length
23226 23325: gap of 100 bp
23326 24072: contig of 747 bp in length
24073 24172: gap of 100 bp
24173 24902: contig of 730 bp in length
24903 25002: gap of 100 bp
25003 25746: contig of 744 bp in length
25747 25846: gap of 100 bp
25847 26585: contig of 739 bp in length
26586 26685: gap of 100 bp
26686 27375: contig of 691 bp in length
27376 27476: gap of 100 bp
27477 28217: contig of 741 bp in length
28218 28317: gap of 100 bp
28319 29039: contig of 722 bp in length
29040 29139: gap of 100 bp
29140 29876: contig of 737 bp in length
29877 29976: gap of 100 bp
29977 30717: contig of 741 bp in length
30718 30817: gap of 100 bp
30818 31554: contig of 737 bp in length
31555 31654: gap of 100 bp
31655 32380: contig of 726 bp in length
32381 32480: gap of 100 bp
32481 33227: contig of 747 bp in length
33228 33327: gap of 100 bp
33328 34072: contig of 745 bp in length
34073 34172: gap of 100 bp
34173 34896: contig of 724 bp in length
34897 34996: gap of 100 bp
34997 35739: contig of 743 bp in length
35740 35839: gap of 100 bp
35840 36559: contig of 720 bp in length
36560 36659: gap of 100 bp
36660 37393: contig of 736 bp in length
37394 37493: gap of 100 bp
37496 38105: contig of 610 bp in length
38106 38205: gap of 100 bp
38206 38948: contig of 743 bp in length
38949 39048: gap of 100 bp
39049 39799: contig of 751 bp in length
39800 39899: gap of 100 bp
39900 40646: contig of 747 bp in length
40647 40746: gap of 100 bp
40747 41467: contig of 721 bp in length
41468 42307: contig of 740 bp in length
42308 42407: gap of 100 bp
42409 43130: contig of 723 bp in length
43131 43230: gap of 100 bp
43231 43963: contig of 733 bp in length
43964 44063: gap of 100 bp
44064 44771: contig of 708 bp in length

FEATURES	Source
LOCUS	DD181590
DEFINITION	DD181590 13869 bp DNA linear PAT 19-DEC-2005
ACCESSION	DD181590
VERSION	DD181590.1 GI:83947781
KEYWORDS	JP 2005514007-A/10.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 13869)
TITLE	Bhatia,U., Tang,I.Y., Elliott,V.S., Tran,U.K., Lee,S.Y., Chang,H., Griffin,U.A., Zheng,W., Blake,J.U., Emertling,B.M., Lee,E.A., Foreysche,I.J., Bulloch,S.A., Lee,S., Reddy,R., Khare,R., Chawla,N.K., Baughn,M.R., Burrill,J.D., Ho,A. and Warren,B.A.
JOURNAL	LIPID-ASSOCIATED MOLECULES
COMMENT	Patent: JP 2005514007-A 10-19-MAY-2005; INCYTE GENOMICS INC, Bridget A WARREN, Brooke M EMERLING, Ernestine A LEE, Hei-n-Ru CHANG, Ian J FORSTYHE, Jennifer A GRIFFIN, Mariah R BAUGHN, Narinder K CHAWLA, Reena KHARE, Roopa REDDY, Sally LEE, Sean A BULLOCH, Soo Yeun LEE, Uyen K TRAN, Vicki S ELLIOTT, Tom Y TANG, Umesh BHATTIA, John D BURRILL, Julie J BLAKE, Anne HO, Wenjin ZHENG
OS	Homo sapiens
PN	JP 2005514007-A/10
PD	19-MAY-2005
PF	19-SEP-2002 JP 2003529924
PR	21-SEP-2001 US 60/324039, 02-NOV-2001 US 60/343876, PR 26-OCT-2001 US 60/346197, 14-DEC-2001 US 60/340223, PR 18-DEC-2001 US 60/342166, 22-JAN-2002 US 60/351562, PR 30-NOV-2001 US 60/334221, 03-MAY-2002 US 60/377576
PI	PI umesh bhatia, tom y tang, vicki s elliot, uyen k tran, soo yeun lee, hei-n-ru chang, jennifer a griffin, wenjin zheng, julie j lee, pi brooke m emertling, ernestine a lee, ian j forsythe, sean a pi bulloch, sally lee, pi roopa reddy, reena khare, narinder k chawla, mariah pi baughn, john pi d burrill, pi anne ho, bridget a warren
CC	CC This description about <220> can't be interpreted CC <220>
CC	CC <221> misc. feature
CC	CC <223> incyte ID No: 3187560CBI
PH	PH Key Location/Qualifiers 1..13869 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

[illegible]

Db 240 AGAAGTGAATCTCGAACCGCATGTCAGAAATGAGTCTAGGCTGTTCTTGAGACC 299
Oy 128 CACACAAGCAGATATTGCTTGTCTTAAGCTAAGCAGTACTGCTCACCTGTG 180
Db 300 CACACGAAAGATATTGCTTGTCTTAAGCTAAGCAGTACTGCTCACCTGTG 352

RESULT 15

AX815990

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches 147, Conservative 1, Mismatches 25, Indels 0, Gaps 0;

66.1%; Score 132.6; DB 2; Length 750;

8 CCTCATCTTTCTAGAGTCTCAAGGCTTCTCATCTTCAAGATCATCTTGGGTGCACACCA 67

Db 180 CCACGTGCTTGGAGAGTCCCAAGGCTTCTCATCTTCAAGATCATCTTGGGTGCACACCA 239

Oy 68 AGAAGTGAATCTCGAACCGCATGTCAGAAATGAGTCTAGGCTGTTCTTGAGACC 127

Db 240 AGAAGTGAATCTCGAACCGCATGTCAGAAATGAGTCTAGGCTGTTCTTGAGACC 299

Oy 128 CACACAAGCAGATATTGCTTGTCTTAAGCTAAGCAGTACTGCTCACCTGTG 180

Db 300 CACACGAAAGATATTGCTTGTCTTAAGCTAAGCAGTACTGCTCACCTGTG 352

Search completed: May 26, 2006, 15:57:00
Job time : 2038 secs

Best Local Similarity 85.5%; Pred. No. 9.9e-32;
Matches 148; Conservative 1; Mismatches 24; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTCTAGTCCCTAAGGCTTCATCCACAGGATCCCGGGTGCACACCA 67
Db 1571 CCACGCTTGAGAGAGTCCCAAGGCTTCATCTCAAGGATCCCTGGGTGCACACCA 1630

Qy 68 AGAAGTGAACCTCGATCTCATGTTTCAGAAATRGAAATGCTCTAGGCTGTTCTTGAGACC 127
Db 1631 AGAAGTGAAGCTCGAACCGCATGTTTCAGAAATRGAAATGCTCTAGGCTGTTCTTGAGACC 1690

Qy 128 CACACAGCAGATATTTGCTTGTCTTAAGCTTAAGCAGTACTGCTCACCCTGTG 180
Db 1691 CACACAGCAGATATTTGCTTGTCTTAAGCTTAAGCAGTACTGCTCACCCTGTG 1743

RESULT 2
CR859622 2798 bp mRNA linear HTC 17-APR-2005
LOCUS Pongo pygmaeus mRNA; cDNA DKFZp470G2422 (from clone DKFZp470G2422).
DEFINITION CR859622
VERSION CR859622.1 GI:55730119
KEYWORDS HTC.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pongo
1 (bases 1 to 2798)
Pousterka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Well, B., Amlid, C., Ossanger, A., Fobo, G., Han, M., and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp470G2422) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneID=DKFZp470G2422
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES
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/note="Plasmin (Homo sapiens)"
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/db_xref="InterPro:IPR000001"
/db_xref="InterPro:IPR001254"
/db_xref="InterPro:IPR001314"
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/db_xref="InterPro:IPR003966"
/db_xref="InterPro:IPR011358"

/db_xref="UniProtKB/TREMBL:Q5R8X6"
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GPMCYTTPBHRDYCDIPCEERACMSQSEBNDGKISKMSGLECAMDSQPHAG
YIPSKFPNKULKKYCNPNDEPRPMFTTDPNKRMLCQIPRTCTPPSSGPNYOC
KGTGENRGNAVAVTSGHTQRMASQIPQTHNRPENPCNDENTCRNDGEKAPM
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PACLPSNVYVARTECFITGMBTQCTFGALLKEQLPTEIKVNRVEFLNGRVK
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FTWIEGVMMNN"

ORIGIN
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Best Local Similarity 85.5%; Pred. No. 1.1e-31;
Matches 148; Conservative 1; Mismatches 24; Indels 0; Gaps 0;

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Qy 68 AGAAGTGAACCTCGATCTCATGTTTCAGAAATRGAAATGCTCTAGGCTGTTCTTGAGACC 127
Db 1956 AGAAGTGAAGCTCGAACCGCATGTTTCAGAAATRGAAATGCTCTAGGCTGTTCTTGAGACC 2015

Qy 128 CACACAGCAGATATTTGCTTGTCTTAAGCTTAAGCAGTACTGCTCACCCTGTG 180
Db 2016 CACACAGCAGATATTTGCTTGTCTTAAGCTTAAGCAGTACTGCTCACCCTGTG 2068

RESULT 3
H73861 424 bp mRNA linear EST 31-OCT-1995
LOCUS ysl2a02.21 Soares fetal liver spleen INFILS Homo sapiens cDNA clone
IMAGE:214538 5' similar to gb:X05199 PLASMINGEN PRECURSOR
(HUMAN); mRNA sequence.
H73861
H73861.1 GI:1046795
EST.
Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 424)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisese, S., Dietrich, N., Dubuque, T., Faveilo, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Roifling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1035
High quality sequence stops: 330
Source: IMAGS Consortium, LNLW
This clone is available royalty-free through LNLW; contact the
IMAGS Consortium (info@image.lnl.gov) for further information.
Insert Length: 1035 Std Error: 0.00
Seq primer: M13RPI

RESULT 12
AV661991
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
SOURCE
ORIGIN
Query Match
Best Local Similarity
Matches

594 bp mRNA linear EST 16-JAN-2002
AV661991 GLC Homo sapiens cDNA clone GLC2G06 3', mRNA sequence.
AV661991 GI:9883005
EST. sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 594)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..594
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/clone="GLC2G06"
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/dev_stage="Adult"
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

66.1%; Score 132.6; DB 1; Length 594;
85.0%; Pred. No. 2.3e-31;
1; Mismatches 25; Indels 0; Gaps 0;

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123 CCACGTGCTTGAGAAATCTCCCAAGGCTTCATCTCAAGGTCATCTGGTGACACCA 182
68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGACC 127
183 AGAAGTGAATCTCGAATCTCGAATCTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGACC 242
128 CACACAGAGATATTTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 180
243 CACACAGAAAGATATTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 295

RESULT 13
AV662084
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
SOURCE
ORIGIN
Query Match
Best Local Similarity
Matches

611 bp mRNA linear EST 16-JAN-2002
AV662084 GLC Homo sapiens cDNA clone GLCHAG06 3', mRNA sequence.
AV662084 GI:9883098
EST. sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 611)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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XhoI"

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1; Mismatches 25; Indels 0; Gaps 0;

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182 AGAAGTGAATCTCGAATCTCGAATCTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGACC 241
128 CACACAGAGATATTTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 180
242 CACACAGAAAGATATTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 294

RESULT 14
B1759134
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
SOURCE
ORIGIN
Query Match
Best Local Similarity
Matches

766 bp mRNA linear EST 25-SEP-2001
B1759134 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183003 5',
mRNA sequence.
B1759134 GI:15750712
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 766)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

66.1%; Score 132.6; DB 1; Length 611;
85.0%; Pred. No. 2.3e-31;
1; Mismatches 25; Indels 0; Gaps 0;

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68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGACC 127
182 AGAAGTGAATCTCGAATCTCGAATCTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGACC 241
128 CACACAGAGATATTTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 180
242 CACACAGAAAGATATTGCTTGTCTAAAGCTAAGCAGTACTGCTCACTGTG 294

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLNL1456 row: 1 column: 12
High quality sequence stop: 766.
Location/Qualifiers

FEATURES
source

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/note="Organ: pooled colon, kidney, stomach; Vector:
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source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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ORIGIN

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Best Local Similarity 85.0%; Pred. No. 2.4e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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OY 128 CACACAAGCAGATATTGCTTCTTAAGCTAAGCAGTACTGCTCACCCTGTG 180
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RESULT 15

LOCUS BG402207 859 bp mRNA linear EST 12-MAR-2001
DEFINITION 602465764F1 NIH_MGC_75 Homo sapiens cDNA IMAGE:4594023 5',
mRNA sequence.

ACCESSION BG402207
VERSION BG402207.1 GI:13295655
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 859)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 629.
Location/Qualifiers

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source

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/clone_11b="NIH_MGC_75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggccatcatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-ATCTAGAGCGCCGAGCGCCGACATG-3' and 3' adaptor sequence:
5'-ATCTAGAGCGCCGAGCGCCGACATG-3' (where B = A, G, C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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ORIGIN

Query Match 66.1%; Score 132.6; DB 2; Length 859;
Best Local Similarity 85.0%; Pred. No. 2.5e-31;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

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OY 68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATGGAAGTGTAGGCTGTTTGGAGCC 127
DB 373 AGAAGTGAATCTCGAAGCCGATGTTCAAGAAATAGAGTGTAGGCTGTTTGGAGCC 432
OY 128 CACACAAGCAGATATTGCTTCTTAAGCTAAGCAGTACTGCTCACCCTGTG 180
DB 433 CACAGGAAAGATATTGCTTCTTAAGCAGTACTGCTCACCCTGTG 485
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Search completed: May 26, 2006, 16:10:41
Job time : 4490 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 12:35:58 ; Search time 354 Seconds
(without alignments)
3958.819 Million cell updates/sec

Title: US-10-796-280-19350
Perfect score: 200.6
Sequence: 1 tctgacctccctccatcttctc.....tcttcacccacgcgtgtga 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database :
1: Genesegq1980s:*
2: Genesegq1980s:*
3: Genesegq2000s:*
4: Genesegq2001as:*
5: Genesegq2001bs:*
6: Genesegq2002as:*
7: Genesegq2002bs:*
8: Genesegq2003as:*
9: Genesegq2003bs:*
10: Genesegq2003cs:*
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14: Genesegq2005s:*
15: Genesegq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	144.4	72.0	820	AA566111	AA566111 DNA encod
5	144.4	72.0	3756	AD038544	Adq38544 Human SNP
6	144.4	72.0	10422	8 ACAG64741	Acag64741 Apolipop
7	144.4	72.0	10422	10 ADF43405	Adf43405 Apolipop
8	144.4	72.0	10422	14 AEA03076	Aea03076 iNOS nucl
9	144.4	72.0	13869	10 ACC49787	Acc49787 Human lip
10	144.4	72.0	13938	8 ACC47280	Acc47280 Human apo
11	144.4	72.0	13938	12 ADO3412	Ado3412 Human apo
12	144.4	72.0	13938	12 ADO75139	Ado75139 Human apo
13	144.4	72.0	13938	13 AD038545	Adq38545 Human SNP
14	132.6	66.2	2178	5 AAS80436	Aae80436 DNA encod
15	132.6	66.1	744	10 ACH00783	Ach00783 Human mic
16	132.6	66.1	750	6 ABR89460	Abn89460 Human mic
17	132.6	66.1	750	10 ACH00782	Ach00782 Human mic
18	132.6	66.1	750	13 ADS20373	AdS20373 Human mic

19	132.6	66.1	783	10 ACH00781	Ach00781 Human mic
20	132.6	66.1	786	10 ACH00780	Ach00780 Human mic
21	132.6	66.1	999	10 ACH00777	Ach00777 Human-S C
22	132.6	66.1	1005	10 ACH00775	Ach00775 Human-S C
23	132.6	66.1	1011	10 ACH00778	Ach00778 Human-S C
24	132.6	66.1	1017	10 ACH00776	Ach00776 Human-S C
25	132.6	66.1	1038	10 ACH00773	Ach00773 Human-S C
26	132.6	66.1	1041	10 ACH00771	Ach00771 Human-S C
27	132.6	66.1	1047	6 ABR89461	Abn89461 Human min
28	132.6	66.1	1047	10 ACH00779	Ach00779 Human min
29	132.6	66.1	1047	13 ADS20377	AdS20377 Human min
30	132.6	66.1	1050	10 ACH00774	Ach00774 Human-S C
31	132.6	66.1	1053	10 ACH00772	Ach00772 Human-S C
32	132.6	66.1	1302	10 ACH00769	Ach00769 Human-S C
33	132.6	66.1	1314	10 ACH00770	Ach00770 Human-S C
34	132.6	66.1	1724	2 AAQ40318	Aaq40318 Sequence
35	132.6	66.1	1907	8 ACC51086	Acc51086 Human Pla
36	132.6	66.1	2145	10 ACH00785	Ach00785 Human Pla
37	132.6	66.1	2236	2 AAQ40258	Aaq40258 Plasmid p
38	132.6	66.1	2236	3 AA89829	Aa89829 Plasmid p
39	132.6	66.1	2296	4 AAS12747	Aas12747 Plasmid p
40	132.6	66.1	2376	10 ACH00784	Ach00784 Human Glu
41	132.6	66.1	2376	13 ADS20379	AdS20379 Human pla
42	132.6	66.1	2400	10 ACH00752	Ach00752 Human-S C
43	132.6	66.1	2412	10 ACH00753	Ach00753 Human-S C
44	132.6	66.1	2430	10 ABR15877	Abx15877 DNA encod
45	132.6	66.1	2432	14 AED76372	Aed76372 Human pla

ALIGNMENTS

RESULT 1	AD045134 standard; DNA; 201 BP.
ID	AD045134
AC	AD045134;
DT	18-NOV-2004 (first entry)
XX	Myocardial infarction-associated SNP flanking transcript, SEQ ID 6797.
DE	Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW	cardiant; gene therapy; human; ds.
XX	Homo sapiens.
OS	WO2004058052-A2.
XX	15-JUL-2004.
PD	22-DEC-2003; 2003WO-US040978.
XX	20-DEC-2002; 2002US-0434778P.
PR	10-MAR-2003; 2003US-0453135P.
PR	30-APR-2003; 2003US-0466412P.
PR	23-SEP-2003; 2003US-0504955P.
XX	(APPL-) ABPLERA CORP.
PA	Cargill M, Devlin JJ, Iakubova O;
PI	WPI; 2004-533949/51.
XX	Identifying an individual who has an altered risk for developing
PT	myocardial infarction by detecting a single nucleotide polymorphism in
PT	the individual's nucleic acids.
XX	Claim 7; SEQ ID NO 6797; 145p; English.
XX	The invention relates to a novel method for identifying an individual who
CC	has an altered risk for developing myocardial infarction. The method
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of

PN WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX P-PSDB; ABG16250.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 16241; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 820 BP; 209 A; 203 C; 209 G; 199 T; 0 U; 0 Other;
SQ
Query Match 72.0%; Score 144.4; DB 5; Length 820;
Best Local Similarity 89.5%; Pred. No. 9.7e-40;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 9 CTCATCTTTTCTAGGCTCTCAAGGCTTCATCTTACAGGTATCTTGGGTGACACCA 68
DB 116 CACTGCTTGAAGAAATCTCAAGGCTTCATCTTCAAGGTATCTTGGGTGACACCA 175
QY 69 GAAGTGAACCTCGAATCTCATGTTTCAGAAATGAGTGTCTAGGCTGTTCTTGAGGCC 128
DB 176 GAAGTGAACCTCGAATCTCATGTTTCAGAAATGAGTGTCTAGGCTGTTCTTGAGGCC 235
QY 129 ACACAAGAGATATTGCTTGTCTAAAGCTAAGCAGGTAAGTCTGCTCACTGTG 180
DB 236 ACACAAGAGATATTGCTTGTCTAAAGCTAAGCAGGCTGCTGCTATCACTG 287
RESULT 4
AAS6111
ID AAS6111 standard; cDNA; 820 BP.
XX
XX AAS6111;
AC
AC AAS6111;
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel human diagnostic protein #1915.

XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX P-PSDB; ABG01924.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 1915; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 820 BP; 209 A; 203 C; 209 G; 199 T; 0 U; 0 Other;
SQ
Query Match 72.0%; Score 144.4; DB 5; Length 820;
Best Local Similarity 89.5%; Pred. No. 9.7e-40;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 9 CTCATCTTTTCTAGGCTCTCAAGGCTTCATCTTCAAGGTATCTTGGGTGACACCA 68
DB 116 CACTGCTTGAAGAAATCTCAAGGCTTCATCTTCAAGGTATCTTGGGTGACACCA 175
QY 69 GAAGTGAACCTCGAATCTCATGTTTCAGAAATGAGTGTCTAGGCTGTTCTTGAGGCC 128
DB 176 GAAGTGAACCTCGAATCTCATGTTTCAGAAATGAGTGTCTAGGCTGTTCTTGAGGCC 235
QY 129 ACACAAGAGATATTGCTTGTCTAAAGCTAAGCAGGTAAGTCTGCTCACTGTG 180
DB 236 ACACAAGAGATATTGCTTGTCTAAAGCTAAGCAGGCTGCTGCTATCACTG 287
RESULT 5
AD038544
ID AD038544 standard; DNA; 3756 BP.

CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidal activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidal activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or moieties. The present
CC sequence encodes an anti-tumour protein which is co-administered with or
CC incorporated into a fusion construct with a superantigen. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from the US patent
CC office website at "seqdata.uspto.gov/sequence.html?docid=20020177551"
CC
XX
SQ Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;
Query Match 72.0%; Score 144.4; DB 8; Length 10422;
Best Local Similarity 89.5%; Pred. No. 3,1e-39;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 9 CTCATCTTTCTAGTCTCTCAAGGCTTCATCTCAAGGTCATCTCTGGTGACACCAA 68
DB 9634 CACTGCTTGAAGAAGTCTCAAGGCTTCATCTCAAGGTCATCTCTGGTGACACCAA 9693
QY 69 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAATGTTCTTGGAGCCC 128
DB 9694 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAATGTTCTTGGAGCCC 9753
QY 129 ACACAAAGCATATTTGCTTCTTAAAGTAAAGCATGCTGCTCACTG 180
DB 9754 ACACAAAGCATATTTGCTTCTTAAAGTAAAGCATGCTGCTCACTG 9805
RESULT 7
ADP43405
ID ADP43405 standard; DNA; 10422 BP.
XX
AC ADP43405;
XX
DT 12-FEB-2004 (first entry)
XX
DE Apolipoprotein polynucleotide seqid 125.
XX
KW receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; apolipoprotein; ds.
XX
XX Unidentified.
XX OS
XX US200315713-A1.
XX PN
XX 21-AUG-2003.
XX PD
XX 28-DEC-2000; 2000US-00751708.
XX PF
XX 28-DEC-1999; 99US-0173371P.
XX PR
XX (TERM/) TERMAN D S.
XX PA
XX Terman DS;
XX PI
XX WPI; 2003-787326/74.
XX DR

DR P-PSDB; ADP43406.
XX
XX New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 125; 151pp; English.
XX PS
XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This sequence represents
CC apolipoprotein polynucleotide, a cell surface moiety, the DNA of which
CC can be transfected into a cell with superantigen DNA to generate
CC antitumour immunity.
CC
XX
SQ Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;
Query Match 72.0%; Score 144.4; DB 10; Length 10422;
Best Local Similarity 89.5%; Pred. No. 3,1e-39;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY 9 CTCATCTTTCTAGTCTCTCAAGGCTTCATCTCAAGGTCATCTCTGGTGACACCAA 68
DB 9634 CACTGCTTGAAGAAGTCTCAAGGCTTCATCTCAAGGTCATCTCTGGTGACACCAA 9693
QY 69 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAATGTTCTTGGAGCCC 128
DB 9694 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAATGTTCTTGGAGCCC 9753
QY 129 ACACAAAGCATATTTGCTTCTTAAAGTAAAGCATGCTGCTCACTG 180
DB 9754 ACACAAAGCATATTTGCTTCTTAAAGTAAAGCATGCTGCTCACTG 9805
RESULT 8
AEA03076
ID AEA03076 standard; DNA; 10422 BP.
XX
AC AEA03076;
XX
DT 28-JUL-2005 (first entry)
XX
DE iNOS nucleotide sequence SEQ ID NO:102.
XX
KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW inducible nitric oxide synthase; gene; ds.
XX
XX Unidentified.
XX OS
XX US2005112141-A1.
XX PN
XX 26-MAY-2005.
XX PD
XX 08-SEP-2004; 2004US-00937758.
XX PF
XX 30-AUG-2000; 2000US-00650884.
XX PR
XX (TERM/) TERMAN D S.
XX PA
XX Terman DS;
XX PI
XX WPI; 2005-394926/40.
XX DR P-PSDB; AEA03077.
XX PF
XX New composition for treating a tumor or neoplastic disease in a subject
PT comprises conjugates comprising superantigen polypeptides or nucleic
PT acids with other molecules that produce a tumoricidal response.
XX
XX Example 3; SEQ ID NO 102; 125pp; English.
XX PS
XX

CC The invention relates to a composition for treating a tumor or neoplastic
CC disease in a subject. Also described: (1) a mammalian cell comprising an
CC exogenous nucleic acid encoding a superantigen expressed in the cell,
CC which cell also produces or expresses all alpha-anomers of
CC monoglycosylceramide or diglycosylceramide, where expression of the
CC superantigen and the mono- or diglycosylceramide is capable of eliciting
CC an antitumor immune response in a mammal into which the cell is
CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
CC preparing a population of immunotherapeutic T or natural killer T (NKT)
CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
CC apoptotic cell preparation or lysate useful for treating a tumor or
CC neoplastic disease in a subject, comprising a cell population that has
CC been transfected with naked DNA encoding a superantigen, and treated to
CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
CC transfected with the above apoptotic preparation or lysate, thus,
CC rendering the cell effective in presenting material expressed from a
CC transfecting nucleic acid or material ingested to the immune system of a
CC mammal to elicit an anti-tumor immune response. The composition and
CC methods are useful for treating tumors or neoplastic diseases. The
CC present sequence represents an INOS nucleotide sequence, which is used in
CC an example from the present invention. Note - The sequence data for this
CC patent is not represented in the printed specification, but was obtained
CC in electronic format directly from the USPTO web site.

XX Sequence 10422 BP; 3020 A; 2386 C; 2503 G; 2513 T; 0 U; 0 Other;

XX Query Match Best Local Similarity 72.0%; Score 144.4; DB 14; Length 10422;

XX Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

XX 9 CTGATCTTTTCTAGTCTCTCAAGGCTTCACTCAAGGTCATCTGGGTGCACACCAA 68

XX 9634 CACTGCTTGAAGAAGTCTCAAGGCTTCACTCAAGGTCATCTGGGTGCACACCAA 9693

XX 69 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAGTGTCTAGGCTGTTCTTGAGAGCC 128

XX 9694 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAGTGTCTAGGCTGTTCTTGAGAGCC 9753

XX 129 ACACAAGCAGATATTTGCTTCTTAAGCTTAAGGCTGCTGCTGCTGCTGCTGCTG 180

XX 9754 ACACAAGCAGATATTTGCTTCTTAAGCTTAAGGCTGCTGCTGCTGCTGCTGCTG 9805

XX Db

XX RESULT 9 ACC49787 standard; cDNA; 13869 BP.

XX ID ACC49787;

XX AC ACC49787;

XX DT 10-JUL-2003 (first entry)

XX Human lipid-associated molecule LIPAM-10 encoding cDNA SEQ ID NO:27.

XX Human, lipid-associated molecule; LIPAM; cytosolic; cerebroprotective;
XX antiarteriosclerotic; anti-HIV; antiallergic; antiparkinsonian; cardiant;
XX anticonvulsant; nootropic; antiinflammatory; antitumor; hepatotropic;
XX antibacterial; virucide; protozoacide; antiparasitic; antipneumatic; AIDS;
XX gene therapy; cell proliferative disease; cancer; atherosclerosis; ulcer;
XX autoimmune disease; inflammatory disease; allergy; neurological disorder;
XX stroke; Parkinson's disease; epilepsy; gastrointestinal disorder;
XX cirrhosis; cardiovascular disorder; myocardial infarction; obesity;
XX metabolic disorder; developmental disorder; endocrine disorder;
XX pulmonary disorder; infection; lipid metabolism disorder; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 46..13692

XX FT /cage a

XX /product= "LIPAM-10"

XX MO2003025150-A2.

XX

PD 27-MAR-2003.

XX 19-SEP-2002; 2002MO-US029980.

XX 21-SEP-2001; 2001US-0324039P.

XX 26-OCT-2001; 2001US-0346197P.

XX 02-NOV-2001; 2001US-0343876P.

XX 30-NOV-2001; 2001US-0344211P.

XX 14-DEC-2001; 2001US-0340233P.

XX 18-DEC-2001; 2001US-0342166P.

XX 22-JAN-2002; 2002US-0351262P.

XX 03-MAY-2002; 2002US-0377576P.

XX (INCY-) INCYTE GENOMICS INC.

XX Warren BA, Emerling BM, Lee EA, Chang H, Forsythe JU, Griffin JA;

XX Baughn MR, Chawla NK, Khare R, Reddy R, Lee S, Bulloch SA, Lee SY;

XX Tran UK, Elliott VS, Tang YT, Bhatia U, Burrill JD, Blake JU, Ho A;

XX Zheng W;

XX WPI; 2003-363142/34.

XX P-PsDB; ABR43305.

XX Claim 5; Page 216-220; 225pp; English.

XX ACC49787 to ACC49794 encode the human lipid-associated molecule proteins
XX given in ABR433296 to ABR433312, designated LIPAM-1 to LIPAM-17 (I). (1)
XX have cytosolic, antiarteriosclerotic, anti-HIV, antiallergic, nootropic,
XX cerebroprotective, antiparkinsonian, anticonvulsant, antiinflammatory,
XX antitumor, hepatotropic, antibacterial, virucide, protozoacide, cardiant,
XX antiparasitic and antipneumatic activities, and can be used in gene
XX therapy. The LIPAM polypeptides and polynucleotides are useful in
XX diagnosing, treating and preventing diseases or conditions associated
XX with decreased expression or overexpression of LIPAM, such as cell
XX proliferative diseases (e.g. cancer or atherosclerosis), autoimmune/
XX inflammatory diseases (e.g. AIDS or allergies), neurological disorders
XX (e.g. stroke, Parkinson's disease or epilepsy), gastrointestinal (e.g.
XX ulcer or cirrhosis), cardiovascular (e.g. myocardial infarction),
XX metabolic (e.g. obesity), developmental, endocrine, or pulmonary
XX disorders, infections (e.g. bacterial, viral, parasitic or protozoal),
XX and disorders of lipid metabolism. They are also useful in assessing the
XX effects of exogenous compounds on the expression of nucleic acid and
XX amino acid sequences of LIPAM. The LIPAMs or their fragments are useful
XX in screening compounds for effectiveness as agonist or antagonist of the
XX polypeptides, or in altering the expression of the target polynucleotide
XX and compounds that specifically bind to or modulate the activity of the
XX polypeptide

XX Sequence 13869 BP; 3589 A; 3879 C; 3551 G; 2850 T; 0 U; 0 Other;

XX Query Match Best Local Similarity 72.0%; Score 144.4; DB 10; Length 13869;

XX Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

XX 9 CTGATCTTTTCTAGTCTCTCAAGGCTTCACTCAAGGTCATCTGGGTGCACACCAA 68

XX 1150 CACTGCTTGAAGAAGTCTCAAGGCTTCACTCAAGGTCATCTGGGTGCACACCAA 13209

XX 69 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAGTGTCTAGGCTGTTCTTGAGAGCC 128

XX 13210 GAAGTGAACCTCGAATCTCATGTTCAAGAAATGAGTGTCTAGGCTGTTCTTGAGAGCC 13269

XX 129 ACACAAGCAGATATTTGCTTCTTAAGCTTAAGGCTGCTGCTGCTGCTGCTGCTG 180

XX 13270 ACACAAGCAGATATTTGCTTCTTAAGCTTAAGGCTGCTGCTGCTGCTGCTG 13321

XX Db

XX RESULT 10 ACC47280

ID ACC47280 standard; DNA, 13938 BP.
XX
XX ACC47280;
AC
XX 11-AUG-2003 (first entry)
DT
XX
XX Human apolipoprotein(a) encoding DNA.
DE
XX
XX Apolipoprotein(a); antiarteriosclerotic; cardiac; gene therapy; human;
KM
XX gene; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 46.13692
FT /*tag= a
FT /product= "apolipoprotein(a)"
XX
XX W02001014307-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024920.
XX
XX 07-AUG-2001; 2001US-00923515.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ;
XX
XX WPI; 2003-256565/25.
XX
XX P-PSDB; ABR39860.
XX
XX New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease.
XX
XX Example 13; Page 92-112, 120pp; English.
XX
XX The invention relates to a new compound, 8-50 nucleobases in length
CC targeted to a nucleic acid molecule encoding human apolipoprotein(a),
CC specifically hybridizes with and inhibits the expression of human
CC apolipoprotein(a). The antisense compounds are useful for preparing a
CC composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a DNA encoding the human apolipoprotein(a) (Genbank accession
CC No. NM_005577)
XX
XX Sequence 13938 BP; 3613 A; 3889 C; 3560 G; 2876 T; 0 U; 0 Other;
SQ
Query Match 72.0%; Score 144.4; DB 8; Length 13938;
Best Local Similarity 89.5%; Pred. No. 3.5e-39;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
OY 9 CTCATCTTTTCAGTCTCCTCAAGGCTTCATCTCAAGATCATCTGAGTGCACACCA 68
DB 13150 CACTCTTGAAGAGAGCTCAAGGCTTCATCTCAAGATCATCTGAGTGCACACCA 13209
OY 69 GAAAGTGAACCTGAAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCTTGAAGCC 128
DB 13210 GAAAGTGAACCTGAAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCTTGAAGCC 13269
OY 129 ACACAGACGATATTTGCTTGTCTAAAGCTAAGACGATCTCGCTACCTGTG 180
DB 13270 ACACAGACGATATTTGCTTGTCTAAAGCTAAGACGCTGCGCTATCACTG 13321
RESULT 11
ADO33412 standard; DNA; 13938 BP.
XX
XX ADO33412;
XX

DT 12-AUG-2004 (first entry)
XX
XX Human apolipoprotein(a) [Lp(a)] DNA - SEQ 860.
DE
XX
XX apolipoprotein B; Apob; cardiovascular; antiarteriosclerotic;
KM antilipemic; antidiabetic; anorectic; cardiac; vasotropic; hypotensive;
KM anabolic; eating disorder; cytostatic; endocrine; vasotropic;
KM neuroprotective; nootropic; lipid; cholesterol metabolism;
KM hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KM Von Gierke's disease; lipodystrophy; Cushing's syndrome;
KM sexual ateliotic dwarfism; hyperthyroidism; hypertension;
KM anorexia nervosa; Werner's syndrome; hepatoma; multiple myeloma; uraemia;
KM impotence; obstructive liver disease; Alzheimer's; dementia; diabetes;
KM obesity; atherosclerosis; human; ds; apolipoprotein(a); Lp(a).
XX
XX Homo sapiens.
OS
XX
XX W02004044181-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036411.
XX
XX 13-NOV-2002; 2002US-0426234P.
XX
XX 15-MAY-2003; 2003WO-US015493.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke R, Graham M, Lemonidis-Tarbet K, Dobbie KM;
XX
XX WPI; 2004-420321/39.
XX
XX Antisense oligonucleotide compound that inhibits expression of mRNA
PT encoding human apolipoprotein B, useful for treating hyperlipidaemia,
PT diabetes, obesity, von Gierke's disease, lipodystrophies, Cushing's
PT syndrome.
XX
XX Example 57; SEQ ID NO 860; 483pp; English.
XX
XX The invention relates to a novel antisense compound where the compound
CC hybridises to and inhibits expression of mRNA encoding human
CC apolipoprotein B (Apob) after 16-24 hours by at least 30% in 80%
CC confluent HepG2 cells in culture at a concentration of 150 nM. The
CC compound of the invention demonstrates cardiovascular,
CC antiarteriosclerotic, antilipemic, antidiabetic, anorectic, cardiac,
CC vasotropic, hypotensive, anabolic, eating disorder-related, cytostatic,
CC endocrine, vasotropic, neuroprotective and nootropic activities and may
CC be useful for inhibiting the expression of apolipoprotein B in cells or
CC tissues in vivo in order to address a condition associated with abnormal
CC lipid or cholesterol metabolism. The compound may be useful for
CC decreasing circulating lipoprotein levels, triglyceride levels,
CC cholesterol levels, lipid levels, fatty acid levels, acute phase
CC reactants and chylomicrons and thus may be utilised during treatment of
CC hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia,
CC cardiovascular disorders, Von Gierke's disease, lipodystrophy, Cushing's
CC syndrome, sexual ateliotic dwarfism, hyperthyroidism, hypertension,
CC anorexia nervosa, Werner's syndrome, hepatoma, multiple myeloma, uraemia,
CC impotence, obstructive liver disease, Alzheimer's disease, dementia,
CC diabetes, obesity and atherosclerosis. The current sequence is that of
CC the human apolipoprotein(a) [Lp(a)] DNA - SEQ ID 860 of the invention.
XX
XX Sequence 13938 BP; 3614 A; 3889 C; 3560 G; 2875 T; 0 U; 0 Other;
SQ
Query Match 72.0%; Score 144.4; DB 12; Length 13938;
Best Local Similarity 89.5%; Pred. No. 3.5e-39;
Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
OY 9 CTCATCTTTTCAGTCTCCTCAAGGCTTCATCTCAAGATCATCTGAGTGCACACCA 68
DB 13150 CACTCTTGAAGAGAGCTCAAGGCTTCATCTCAAGATCATCTGAGTGCACACCA 13209
OY 69 GAAAGTGAACCTGAAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCTTGAAGCC 128

Db 13310 GAAGTGAACCTCGATCTCATGTTTCAGGAATGAGTGTCTAGGCTGTTCTTGAGCCC 13269

Qy 129 ACACAGAGATATTGCTTCTTAAGCTAAGCAGTACTGCTCACCCTGTG 180
 |||||
 Db 13270 ACACAGAGATATTGCTTCTTAAGCTAAGCAGGCGCTGCATCATCAGC 13321

RESULT 12
 ADQ75139
 ID ADQ75139 standard; CDNA; 13938 BP.

XX AC ADQ75139;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human apolipoprotein A cDNA.

XX cardiovaseular; antiatherosclerotic; antilipemic; vasotropic;
 KM apolipoprotein modulator A; apolipoprotein A; plasminogen;
 KM apolipoprotein A associated disorder; cardiovascular disorder;
 KM atherosclerosis; hypercholesterolaemia; coronary artery disease; human;
 KM gene; ss.

XX Homo sapiens.
 XX
 PN US2004138164-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 15-OCT-2003; 2003US-00684440.
 XX
 PR 07-AUG-2001; 2001US-00923515.
 PR 02-JUN-2003; 2003US-0475402P.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Crooke RM, Graham MJ;
 XX
 PT WPI; 2004-533399/51.
 DR P-PSDB; ADQ75209.
 XX
 PT New antisense oligonucleotide compounds, useful for diagnosing,
 PT preventing and/or treating conditions with aberrant expression of
 PT apolipoprotein(a), such as atherosclerosis, hypercholesterolemia and
 PT coronary artery disease.

XX
 XX Example 13; SEQ ID NO 4; 54bp; English.

XX The invention describes a new compound (I) comprising 8-80 nucleobases in
 CC length targeted to a nucleic acid molecule encoding apolipoprotein(a),
 CC where the compound is at least 70% complementary to the nucleic acid
 CC molecule encoding apolipoprotein(a), and inhibits the expression of
 CC apolipoprotein(a) mRNA by at least 10%. Also described are: a method of
 CC inhibiting the expression of apolipoprotein(a) in cells or tissues; a
 CC method of treating an animal having a disease or condition associated
 CC with apolipoprotein(a); a method of screening for a modulator of
 CC apolipoprotein(a); a diagnostic method for identifying a disease state,
 CC comprising identifying the presence of apolipoprotein(a) in a sample
 CC using at least one of the primers selected from a fully defined sequence
 CC of 25, 18 or 24 bp (SEQ ID NO: 5, 6 or 7) as given in the specification;
 CC a kit or assay device comprising (I); and a method of inhibiting the
 CC expression of apolipoprotein(a), comprising contacting a biological
 CC system expressing human apolipoprotein(a) with a synthetic antisense
 CC compound, where the synthetic antisense compound comprises 15-30
 CC nucleobases in length and has at least 3 mismatches to human plasminogen.
 CC The methods and compositions of the present invention are useful for the
 CC diagnosis, prevention and/or treatment of diseases or conditions
 CC associated with aberrant expression or activity of apolipoprotein(a),
 CC such as cardiovascular disorder, atherosclerosis, hypercholesterolaemia,
 CC coronary artery disease and/or their combinations. This sequence encodes
 CC human apolipoprotein A.

XX
 XX Sequence 13938 BP; 3613 A; 3889 C; 3560 G; 2876 T; 0 U; 0 Other;

Query Match 72.0%; Score 144.4; DB 12; Length 13938;
 Best Local Similarity 89.5%; Pred. No. 3.5e-39;
 Matches 154; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

Qy 9 CTGATCTTTTCTAGTCCCTTAAGGCTTCATCCCTACAGAGGTCATCCGGGACACCCAA 68
 |||||
 Db 13150 CATGCTGAAGAAGTCTCAAGGCTTCATCTCAAGAGGATCTGCGGACACCAA 13209

Qy 69 GAAGTGAACCTCGATCTCATGTTTCAGGAATGAGTGTCTAGGCTGTTCTTGAGCCC 128
 |||||
 Db 13210 GAAGTGAACCTCGATCTCATGTTTCAGGAATGAGTGTCTAGGCTGTTCTTGAGCCC 13269

Qy 129 ACACAGAGATATTGCTTCTTAAGCTAAGCAGTACTGCTCACCCTGTG 180
 |||||
 Db 13270 ACACAGAGATATTGCTTCTTAAGCTAAGCAGGCGCTGCATCATCAGC 13321

RESULT 13
 ADQ38545
 ID ADQ38545 standard; DNA; 13938 BP.

XX AC ADQ38545;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 208.
 XX
 KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KM cardiant; gene therapy; human; gene; de.

XX Homo sapiens.
 OS
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ, Iakubova O;
 XX
 PT WPI; 2004-533949/51.
 DR P-PSDB; ADQ39373.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.

XX
 XX Claim 7; SEQ ID NO 208; 145bp; English.

XX The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a

CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiac activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 13938 BP; 3611 A; 3880 C; 3553 G; 2873 T; 0 U; 21 Other;

Query Match 72.0%; Score 144.4; DB 13; Length 13938;
Best Local Similarity 90.1%; Pred. No. 3.5e-39;
Matches 155; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 9 CTCATCTTTCTAGGCTCTCAAGGCTTCATCTCTACAGATCATCTGGTGACACCA 68
DB 13150 CACTGCTTGAAGAGTCTCTCAAGGCTTCATCTCTACAGATCATCTGGTGACACCA 13209
OY 69 GAAGTGAACCTCGAATCTCATGTTTCAGGAAATRGAAATGCTTACGCTTCTTGGAGCCC 128
DB 13210 GAAGTGAACCTCGAATCTCATGTTTCAGGAAATRGAAATGCTTACGCTTCTTGGAGCCC 13269
OY 129 ACACAGAGATATTTGCTTCTTAAAGCTACAGAGCTACTGGCTACCTGTG 180
DB 13270 ACACAGAGATATTTGCTTCTTAAAGCTACAGAGCTACTGGCTACCTGTG 13321

RESULT 14

AAS80436/C
ID AAS80436 standard; cDNA, 2178 BP.

XX AAS80436;

XX 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #16240.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Dymanac RT, Liu C, Tang YT,

XX WPI, 2001-639362/73.

DR P-PSDB; ABG16249.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 1; SEQ ID NO 16240; 103BP; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (II) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2178 BP; 453 A; 532 C; 574 G; 619 T; 0 U; 0 Other;

Query Match 66.2%; Score 132.8; DB 5; Length 2178;
Best Local Similarity 88.3%; Pred. No. 1.7e-35;
Matches 143; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

OY 19 CTAGTCTCTCAAGGCTTCATCTCTACAGATCATCTGGTGACACCAAGATGATC 78
DB 272 CAAGTCTCTCAAGGCTTCATCTCTACAGATCATCTGGTGACACCAAGATGATC 213
OY 79 TCGAATCTCATGTTTCAGGAAATRGAAATGCTTACGCTTCTTGGAGCCCACAGCAG 138
DB 212 TCGAATCTCATGTTTCAGGAAATRGAAATGCTTACGCTTCTTGGAGCCCACAGCAG 153
OY 139 ATATTGCTTGTCTAAGCTTAAGCAGATGATCTGCTACCTGTG 180
DB 152 ATATTGCTTGTCTAAGCTTAAGCAGATGATCTGCTGCGGCTCATCATCTG 111

RESULT 15

ACH00783
ID ACH00783 standard; DNA; 744 BP.

XX ACH00783;

XX 12-FEB-2004 (first entry)

DE Human micro-plasminogen gene SEQ ID NO: 64.

XX Recombinant protein production; plasminogen; signal peptide;

KM plasminogen activator identification; protease; wound healing; vulnery;

KM anticoagulant; thrombolytic; cardiac; cerebroprotective; vasotropic;

XX antiinflammatory; ophthalmological; thrombosis; gene; ds.

OS Homo sapiens.

PN WO2003066842-A2.

PD 14-AUG-2003.

PR 06-FEB-2003; 2003WO-DE000341.

PR 06-FEB-2002; 2002EP-00002716.

PR 21-FEB-2002; 2002US-0357809P.

XX (TROM-) TROMMSDORFF ARZNEIMITTEL GMBH & CO KG.

XX Susilo R, Korting HC, Gassen HG, Hils M, Pasternack R,

XX WPI, 2003-697451/66.

PT Recombinant production of plasminogen as a fusion protein comprising a
PT signal peptide that can be removed by proteolysis is useful as an
PT antithrombotic and anticoagulant.

PS Claim 25; Page 68-69; 140pp; German.

XX
CC The present invention relates to a method of producing a recombinant
CC functional plasminogen in microorganisms. The method comprises a sequence
CC encoding at least a functional part of such a plasminogen and a sequence
CC encoding a signal peptide that are fused together, where the two
CC sequences are linked through codons that encode a protease cleavage site
CC to allow removal of the signal peptide. The plasminogen is used to screen
CC for plasminogen activators. Both plasminogen and plasmin, prepared from
CC it by activation, are used for treatment of wounds and the
CC treatment/prevention of thrombotic events, including use in wound
CC dressings, as antithrombotic and anticoagulant agents for preventing or
CC treating a wide variety of conditions, e.g. cardiac infarct, stroke,
CC thrombosis, restenosis, hypoxia, ischemia, vascular inflammation,
CC pulmonary embolism, conjunctivitis (plasminogen type-I deficiency), burns
CC and disseminated intravascular coagulation. The present sequence is a
CC coding sequence used in the exemplification of the invention
XX
SQ Sequence 744 BP; 177 A; 169 C; 207 G; 191 T; 0 U; 0 Other;

Query Match 66.1%; Score 132.6; DB 10; Length 744;

Best Local Similarity 85.0%; Pred. No. 1.3e-35;

Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY	8	CCTCATCTTTCTAGTCTCAAGGCTTCATCTTACAGGTGATCTGGGTGCACACA	67
DB	174	CCACTGCTTGAGAGAGTCCCAAGCCTTCATCTTACAGGTGATCTGGGTGCACACA	233
QY	68	AGAAAGTGAACCTGCAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTTGAAGCC	127
DB	234	AGAAAGTGAATCTCGAACCGCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTTGAAGCC	293
QY	128	CACACAGCAGATATGCTGCTTAAGCTTAAGCAGGTACTGGCTCACTGTG	180
DB	294	CACACGAAAAGATATGCTGCTTAAGCTTAAGCAGGTACTGGCTCACTGTG	346

Search completed: May 26, 2006, 14:14:02
Job time : 357 secs

RESULT 2
US-09-949-016-15854
; Sequence 15854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15854
; LENGTH: 55195
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15854

Query Match 92.8%; Score 186.2; DB 3; Length 55195;
Best Local Similarity 95.0%; Pred. No. 9.3e-54;
Matches 191; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTGACATCTCTCATCTTTTCTAGTCTCTCAAGCCTTCACTCAAGAGTCATCTCTGGTG 60
DB 38902 TTGACGCTCTCATCTTTTCTAGTCTCTCAAGCCTTCACTCAAGAGTCATCTCTGGTG 38961
QY 61 CACACCAAGAGTGAACCTCGATCTCATGTTCAAGAAATGAGTCTAGCTGTCT 120
DB 38962 CACACCAAGAGTGAATCTCGAAGCCGATGTTCAAGAAATGAGTCTAGCTGTCT 39021
QY 121 TGGAGCCCAACACAGATATGCTGCTTAAAGCTAAGAGTCTGCTACCTGTG 180
DB 39022 TGGAGCCCAACAGAAATATGCTGCTTAAAGCTAAGAGTCTGCTACCTGTG 39081
QY 181 GTCTTCACCCCAAGCTGTGGA 201
DB 39082 GTCTTCACCCCAAGCTGTGGA 39102

RESULT 3
5200340-5
; Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINDEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987
; SEQ ID NO: 5
; LENGTH: 1724
5200340-5

Query Match 66.1%; Score 132.6; DB 10; Length 1724;
Best Local Similarity 85.0%; Pred. No. 8.9e-36;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTATCTTTTCTAGTCTCTCAAGCCTTCACTCAAGAGTCTAGCTGTGACACCA 67
DB 1086 CCATGCTTGAAGAGTCCCAAGGCTTCACTCAAGAGTCTAGCTGTGACACCA 1145
QY 68 AGAAGTGAACCTGGAATCTCATGTTCAAGAAATGAGTCTAGGCTGTTTGGAGCC 127
DB 1146 AGAATGAATCTGGAACCGCATGTTCAAGAAATGAGTCTAGGCTGTTTGGAGCC 1205

QY 128 CACACAGCAGATATGCTTCTTAAGCTAAGAGTCTAGCTGTG 180
DB 1206 CACACAGAAATATGCTTCTTAAGCTAAGAGTCTAGCTGTG 1258

RESULT 4
US-10-000-489-53
; Sequence 53, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 53
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1043
; NAME/KEY: CDS
; LOCATION: 1044..1664
; NAME/KEY: 3'UTR
; LOCATION: 1665..1907
; NAME/KEY: polyA signal
; LOCATION: 1869..1874
; NAME/KEY: polyA site
; LOCATION: 1892..1907
US-10-000-489-53

Query Match 66.1%; Score 132.6; DB 3; Length 1907;
Best Local Similarity 85.0%; Pred. No. 9.3e-36;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTATCTTTTCTAGTCTCTCAAGCCTTCACTCAAGAGTCTAGCTGTGACACCA 67
DB 1097 CCATGCTTGAAGAGTCCCAAGGCTTCACTCAAGAGTCTAGCTGTGACACCA 1156
QY 68 AGAAGTGAACCTGGAATCTCATGTTCAAGAAATGAGTCTAGGCTGTTTGGAGCC 127
DB 1157 AGAAGTGAATCTCAAGCGCATGTTCAAGAAATGAGTCTAGGCTGTTTGGAGCC 1216
QY 128 CACACAGCAGATATGCTTCTTAAGCTAAGAGTCTAGCTGTG 180
DB 1217 CACACAGAAATATGCTTCTTAAGCTAAGAGTCTAGCTGTG 1269

RESULT 5
US-09-992-095B-53
; Sequence 53, Application US/0992095B
; Patent No. 6989262
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US.DIV

CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Jpatent
SEQ ID NO 53
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1043
FEATURE:
NAME/KEY: CDS
LOCATION: 1044..1664
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1665..1907
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1869..1874
FEATURE:
NAME/KEY: polyA site
LOCATION: 1892..1907
US-09-992-095B-53

Query Match 66.1%; Score 132.6; DB 4; Length 1907;
Best Local Similarity 85.0%; Pred. No. 9,3e-36;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTCTAGGCTCTCAAGGCTTCTCATCTCAAGGCTCCTGGGTGACACCA 67
Db 1097 CCACTGCTTGAGAGAGTCCCAAGGCTTCTCATCTCAAGGCTCCTGGGTGACACCA 1156
Qy 68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTTTTGGAGCC 127
Db 1157 AGAAGTGAATCTCGAAGCGCATGTTCAAGAAATGAAAGTGTCTAGGCTTTTGGAGCC 1216
Qy 128 CACACAGCAGATATTGCTTCTTAAAGCTAAGCAGGTAATCGCTCACCTGTG 180
Db 1217 CACACGAAAGATATTGCTTCTTAAAGCTAAGCAGGTAATCGCTCACCTGTG 1269

RESULT 6
US-10-000-986A-53
Sequence 53, Application US/10000986A
Patent No. 7005500
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephanie
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-0910509D1V
CURRENT APPLICATION NUMBER: US/10/000,986A
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Jpatent
SEQ ID NO 53
LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1043
FEATURE:
NAME/KEY: CDS
LOCATION: 1044..1664
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 1665..1907
FEATURE:
NAME/KEY: polyA signal
LOCATION: 1869..1874
FEATURE:
NAME/KEY: polyA site
LOCATION: 1892..1907
US-10-000-986A-53

Query Match 66.1%; Score 132.6; DB 5; Length 1907;
Best Local Similarity 85.0%; Pred. No. 9,3e-36;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTCTAGGCTCTCAAGGCTTCTCATCTCAAGGCTCCTGGGTGACACCA 67
Db 1097 CCACTGCTTGAGAGAGTCCCAAGGCTTCTCATCTCAAGGCTCCTGGGTGACACCA 1156
Qy 68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTTTTGGAGCC 127
Db 1157 AGAAGTGAATCTCGAAGCGCATGTTCAAGAAATGAAAGTGTCTAGGCTTTTGGAGCC 1216
Qy 128 CACACAGCAGATATTGCTTCTTAAAGCTAAGCAGGTAATCGCTCACCTGTG 180
Db 1217 CACACGAAAGATATTGCTTCTTAAAGCTAAGCAGGTAATCGCTCACCTGTG 1269

RESULT 7
US-07-750-080A-18
Sequence 18, Application US/07750080A
Patent No. 5445953
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 IMMUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: pN29pc-LPg (Fig. 5.3)
US-07-750-080A-18

Query Match 66.1%; Score 132.6; DB 2; Length 2296;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTATCTTTTCTAGTCTCAAGGCTTCATCTCAAGGTCATCTCGGTGACACCA 67
DB 1652 CCACTGCTTGAGAGATCCCAAGGCTTCATCTCAAGGTCATCTCGGTGACACCA 1711

QY 68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCC 127
DB 1712 AGAAGTGAATCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCC 1771

QY 128 CACACAGCAGATATTGCTTGTCTTAAGCTTAAGCAGAGTACTCGCTCACTGTG 180
DB 1772 CACACGAAAAGATATTGCTTGTCTTAAGCTTAAGCAGAGTACTCGCTCACTGTG 1824

RESULT 8
US-08-651-472-18
Sequence 18, Application US/08651472
Patent No. 6103244
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651.472
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pN29pc-LPg
US-08-651-472-18

Query Match 66.1%; Score 132.6; DB 3; Length 2296;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTATCTTTTCTAGTCTCAAGGCTTCATCTCAAGGTCATCTCGGTGACACCA 67
DB 1652 CCACTGCTTGAGAGATCCCAAGGCTTCATCTCAAGGTCATCTCGGTGACACCA 1711

QY 68 AGAAGTGAACCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCC 127
DB 1712 AGAAGTGAATCTCGAATCTCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCC 1771

QY 128 CACACAGCAGATATTGCTTGTCTTAAGCTTAAGCAGAGTACTCGCTCACTGTG 180
DB 1772 CACACGAAAAGATATTGCTTGTCTTAAGCTTAAGCAGAGTACTCGCTCACTGTG 1824

RESULT 9
US-08-358-928-18
Sequence 18, Application US/08358928
Patent No. 6265183
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FLEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358.928
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pN29pt-Lp9
US-08-358-928-18

Query Match 66.1%; Score 132.6; DB 3; Length 2296;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTCATCTTTCTAGGCTCTCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 67
DB 1652 CCACGTGCTTGAGAGATGCCCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 1711
QY 68 AGAAGTGAACCTCGAATCTCATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 127
DB 1712 AGAAGTGAATCTCGAATCCGATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 1771
QY 128 CACACAAGCAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 180
DB 1772 CACACGAAAAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 1824

RESULT 10
US-09-192-012-4
Sequence 4, Application US/09192012A
Patent No. 6475784
GENERAL INFORMATION:
APPLICANT: Parkeoff, Jackie
APPLICANT: Megabios Corporation
APPLICANT: Pfizer, Inc.
TITLE OF INVENTION: Inhibition of Angiogenesis by Delivery of Nucleic Acids
TITLE OF INVENTION: Encoding Anti-Angiogenic Polypeptides
FILE REFERENCE: 018484-000110US
CURRENT APPLICATION NUMBER: US/09/192, 012A
EARLIER FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: US 60/066, 020
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 2430
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) -(2430)
OTHER INFORMATION: human plasminogen
US-09-192-012-4

Query Match 66.1%; Score 132.6; DB 3; Length 2430;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTCATCTTTCTAGGCTCTCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 67
DB 1863 CCACGTGCTTGAGAGATGCCCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 1922
QY 68 AGAAGTGAACCTCGAATCTCATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 127
DB 1923 AGAAGTGAATCTCGAATCCGATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 1982
QY 128 CACACAAGCAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 180

DB 1983 CACACGAAAAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 2035

RESULT 11
US-08-643-219-12
Sequence 12, Application US/08643219
Patent No. 5801146
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643, 219
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Diane
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-643-219-12

Query Match 66.1%; Score 132.6; DB 2; Length 2497;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 8 CCTCATCTTTCTAGGCTCTCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 67
DB 1912 CCACGTGCTTGAGAGATGCCCAAGGCTTCATCTCTAAGATCATCTGGGTGCACACCA 1971
QY 68 AGAAGTGAACCTCGAATCTCATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 127
DB 1972 AGAAGTGAATCTCGAATCCGATGTTTCAGAAATGGAAGTGTCTAGGCTGTTCTTGAGCC 2031
QY 128 CACACAAGCAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 180
DB 2032 CACACGAAAAGATATTCCTTGTCTTAAAGCTTAAAGAGTACTCGCTCACCTGTG 2084

RESULT 12
US-09-131-995-12
Sequence 12, Application US/09131995
Patent No. 5972896
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,995
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Diane
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-131-995-12

Query Match 66.1%; Score 132.6; DB 2; Length 2497;
Best Local Similarity 85.0%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 147; Conservative 1; Mismatches 25;
Qy 8 CCTCATCTTTCTAGTCTCAAGGCTTCATCTCTACAGGCTTCCTGGGTGACACCA 67
Db 1912 CCATGCTTGAGAGAGTCCCAAGGCTTCATCTCTACAGGCTTCGGGTGACACCA 1971
Qy 68 AGAAGTGAACCTCGATCTCATGTTCAGAAATRGAAAGTGTCTAGGCTGTTCTTGAGACC 127
Db 1972 AGAAGTGAATCTCGAAGCGCATGTTCAAGAAATAGAGTGTCTAGGCTGTTCTTGAGACC 2031
Qy 128 CACACAGCAGATTTGCTTGGCTTAAAGCTAAGCAGGTACTGCTCACCCTGTG 180
Db 2032 CACACGAAAAGATATTTGCTTGAAGCTAAGCAGTCTGCGGTCACTACTG 2084

RESULT 13
US-08-832-087B-12
Sequence 12, Application US/08832087B
Patent No. 5981484
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087B
FILING DATE: 03-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Diane
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-832-087B-12

Query Match 66.1%; Score 132.6; DB 2; Length 2497;
Best Local Similarity 85.0%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 147; Conservative 1; Mismatches 25;
Qy 8 CCTCATCTTTCTAGTCTCAAGGCTTCATCTCTACAGGCTTCCTGGGTGACACCA 67
Db 1912 CCATGCTTGAGAGAGTCCCAAGGCTTCATCTCTACAGGCTTCGGGTGACACCA 1971
Qy 68 AGAAGTGAACCTCGATCTCATGTTCAGAAATRGAAAGTGTCTAGGCTGTTCTTGAGACC 127
Db 1972 AGAAGTGAATCTCGAAGCGCATGTTCAAGAAATAGAGTGTCTAGGCTGTTCTTGAGACC 2031
Qy 128 CACACAGCAGATTTGCTTGGCTTAAAGCTAAGCAGGTACTGCTCACCCTGTG 180
Db 2032 CACACGAAAAGATATTTGCTTGAAGCTAAGCAGTCTGCGGTCACTACTG 2084

RESULT 14
US-08-851-350-12
Sequence 12, Application US/08851350
Patent No. 6057122
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Casuco, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940 US, P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-2137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-350-12

Query Match 66.1%; Score 132.6; DB 3; Length 2497;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTCTAGTCTCAAGGCTTCAATCTTCAAGGTCTCTGGGTGACACCA 67
Db 1912 CCATGCTTGAGAGATGCCCAAGGCTTCAATCTTCAAGGTCTCTGGGTGACACCA 1971

Qy 68 AGAAGTGAACCTCGAATCTCATCTTCAAGAAATGAAATGCTTCTGGGTGACACCA 127
Db 1972 AGAAGTGAATCTCGAATCTCGAATGTTTCAAGAAATGAAATGCTTCTGGGTGACACCA 2031

Qy 128 CACACAAGCAGATATGCTGCTTAAAGCTAAGCAGGTAAGTCTGCTACCTGTG 180
Db 2032 CACACGAAAAGATATGCTGCTTAAAGCTAAGCAGGTAAGTCTGCTACCTGTG 2084

RESULT 15
US-09-132-154-12
Sequence 12, Application US/09132154
Patent No. 6251867
GENERAL INFORMATION:
APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pasteo Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,154
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,087
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Casuco, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940 US, P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-132-154-12

Query Match 66.1%; Score 132.6; DB 3; Length 2497;
Best Local Similarity 85.0%; Pred. No. 1e-35;
Matches 147; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 8 CCTCATCTTTCTAGTCTCAAGGCTTCAATCTTCAAGGTCTCTGGGTGACACCA 67
Db 1912 CCATGCTTGAGAGATGCCCAAGGCTTCAATCTTCAAGGTCTCTGGGTGACACCA 1971

Qy 68 AGAAGTGAACCTCGAATCTCATCTTCAAGAAATGAAATGCTTCTGGGTGACACCA 127
Db 1972 AGAAGTGAATCTCGAATCTCGAATGTTTCAAGAAATGAAATGCTTCTGGGTGACACCA 2031

Qy 128 CACACAAGCAGATATGCTGCTTAAAGCTAAGCAGGTAAGTCTGCTACCTGTG 180
Db 2032 CACACGAAAAGATATGCTGCTTAAAGCTAAGCAGGTAAGTCTGCTACCTGTG 2084

Search completed: May 26, 2006, 13:54:15
Job time : 96 secs

RESULT 2
US-10-995-561-25501
Sequence 25501, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25501
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-25501

Query Match 100.0%; Score 200.6; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 4,5e-61;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 60
DB 1 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 60
QY 61 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 120
DB 61 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 120
QY 121 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 180
DB 121 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 180
QY 181 GTCTTACCCCAAGCTGTGA 201
DB 181 GTCTTACCCCAAGCTGTGA 201

RESULT 3
US-11-124-368A-8354/C
Sequence 8354, Application US/11124368A
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8354
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-368A-8354

Query Match 100.0%; Score 200.6; DB 15; Length 201;
Best Local Similarity 100.0%; Pred. No. 4,5e-61;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 60
DB 201 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 142

QY 61 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 120
DB 141 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 82
QY 121 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 180
DB 81 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 22
QY 181 GTCTTACCCCAAGCTGTGA 201
DB 21 GTCTTACCCCAAGCTGTGA 1

RESULT 4
US-10-741-600-17618
Sequence 17618, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17618
LENGTH: 93112
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(93112)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables:
US-10-741-600-17618

Query Match 100.0%; Score 200.6; DB 9; Length 93112;
Best Local Similarity 100.0%; Pred. No. 5,6e-60;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 60
DB 78990 TTGACATCTCATCTTTTCTAGGTCCTCAAGGCTTCATCTCAAGGTCATCTGGGTG 79049
QY 61 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 120
DB 79050 CACACCAAGAGTGAAGTGAATCTCATCTTCAAGGAAATGAAATGATCTAGGCTGTCT 79109
QY 121 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 180
DB 79110 TGAAGCCCAACACAGAGATATTCCTTGAAGTCAAGAGTACTGCTCACTGTG 79169
QY 181 GTCTTACCCCAAGCTGTGA 201
DB 79170 GTCTTACCCCAAGCTGTGA 79190

RESULT 5
US-10-995-561-13234
Sequence 13234, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13234

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/
/   LENGTH: 93112
/   TYPE: DNA
/   ORGANISM: Homo sapiens
/   FEATURE:
/   NAME/KEY: misc_feature
/   LOCATION: (1)...(93112)
/   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-113234
```

```
Query Match      100.0%; Score 200.6; DB 10; Length 93112;
Best Local Similarity 100.0%; Pred. No. 5.6e-60;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TTGACATCCCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 60
DB TTACATCTCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 79049
QY 61 CACACCAAGAGTGAACCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 120
DB CACACCAAGAGTGAACCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 79109
QY 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 180
DB 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 79169
QY 181 GTCTTACCCCAAGCTGTGTA 201
DB 79170 GTCTTACCCCAAGCTGTGTA 79190
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RESULT 6

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US-09-925-065A-869309/c
/ Sequence 869309, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 869309
/ LENGTH: 614
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-869309
```

```
Query Match      93.4%; Score 187.4; DB 4; Length 614;
Best Local Similarity 95.0%; Pred. No. 3.8e-56;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 TTGACATCCCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 60
DB 406 TTGACATCCCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 347
QY 61 CACACCAAGAGTGAACCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 120
DB 346 CACACCAAGAGTGAATCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 287
QY 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 180
DB 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 180
```

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DB 286 TGAAGCCCAACAAGAAATATTGCTTCTTAAGCTAAGCAGTACTCGTTCACCTGTG 227
QY 181 GTCTTACCCCAAGCTGTGTA 201
DB 226 GTCTTACCCCAAGCTGTGTA 206
```

RESULT 7

```
US-09-925-065A-886262/c
/ Sequence 886262, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 886262
/ LENGTH: 614
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-886262
```

```
Query Match      93.4%; Score 187.4; DB 4; Length 614;
Best Local Similarity 95.0%; Pred. No. 3.8e-56;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 TTGACATCCCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 60
DB 406 TTGACATCCCTCATCTTTCTTAGGCTCTCAAGGCTTCATCTCAAGGTCATCTGGGTTG 347
QY 61 CACACCAAGAGTGAACCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 120
DB 346 CACACCAAGAGTGAATCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTCT 287
QY 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 180
DB 121 TGAAGCCCAACAAGAGATATTGCTTCTTGAAGCTTAAGCAGTACTCGCTCACTGTG 227
QY 181 GTCTTACCCCAAGCTGTGTA 201
DB 226 GTCTTACCCCAAGCTGTGTA 206
```

RESULT 8

```
US-09-925-065A-869309/c
/ Sequence 869309, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
```

PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 869309
LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-869309

Query Match 93.4%; Score 187.4; DB 5; Length 614;
Best Local Similarity 95.0%; Pred. No. 3.8e-56;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 60
DB 406 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 347
QY 61 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 120
DB 346 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 287
QY 121 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 180
DB 286 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 227
QY 181 GTCTTCAACCCACGCTGTGTA 201
DB 226 GTCTTCAACCCACGCTGTGTA 206

RESULT 9
US-09-925-065A-886262/c
Sequence 886262, Application US/09925065A
Publication No. US2005028172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 886262
LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-886262

Query Match 93.4%; Score 187.4; DB 5; Length 614;
Best Local Similarity 95.0%; Pred. No. 3.8e-56;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 60
DB 406 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 347
QY 61 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 120

DB 346 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 287
QY 121 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 180
DB 286 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 227
QY 181 GTCTTCAACCCACGCTGTGTA 201
DB 226 GTCTTCAACCCACGCTGTGTA 206

RESULT 10
US-10-741-601-5650
Sequence 5650, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 5650
LENGTH: 63693
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-5650

Query Match 93.4%; Score 187.4; DB 8; Length 63693;
Best Local Similarity 95.0%; Pred. No. 2.6e-55;
Matches 191; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 60
DB 42930 TTGACATCTCATCTTTTCTAGTCTCTCAAGGCTTCACTTCAAGGTCATCTGGGTG 42989
QY 61 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 120
DB 42990 CACACCAAGAGTGAATCTCAATCTCAATCTCAAGGTAATGAGTGTCTAGGCTGTCT 43049
QY 121 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 180
DB 43050 TGGAGCCCAACAGAGATATGCTTGAAGGCTTAAAGGTAAGGTAAGGTAAGGTAAGG 43109
QY 181 GTCTTCAACCCACGCTGTGTA 201
DB 43110 GTCTTCAACCCACGCTGTGTA 43130

RESULT 11
US-10-995-561-13269
Sequence 13269, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 13269
LENGTH: 63693
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13269

Query Match 93.4%; Score 187.4; DB 10; Length 63693;
Best Local Similarity 95.0%; Pred. No. 2.6e-55;

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New);
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: Patentin version 3.3
;; SEQ ID NO 15327
;; LENGTH: 889
;; TYPE: DNA
;; ORGANISM: Glycine max
US-10-953-349-15327

Query Match 15.0%; Score 30; DB 6; Length 889;
Best Local Similarity 53.6%; Pred. No. 0.27; 51; Indels 0; Gaps 0;
Matches 60; Conservative 1; Mismatches 51; Indels 0; Gaps 0;

OY 49 TCATCCGGGTCACACCAAGAGTGAACCTGATCTCATGTTGAGAAATGGAAGTGT 108
DB 694 TCATCACCCTGACACAGGAGAGGGAATCTGAAATTAATTTTCAAACTAAGAGT 753
OY 109 CTAGGCTGTTCTTGAGCCACACAGCAGATATTGCTTGAAGCTAAG 160
DB 754 GAAGCTTGTTTGAATGAAATTTGTTGAGTTGTCATATTATCATATAG 805

RESULT 3
US-11-293-697-471
;; Sequence 471, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 471
;; LENGTH: 3038
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-471

Query Match 13.9%; Score 27.8; DB 7; Length 3038;
Best Local Similarity 50.4%; Pred. No. 2.6;
Matches 65; Conservative 1; Mismatches 63; Indels 0; Gaps 0;

OY 34 CTTCATCTTACAAAGTCATCTGCGTGACACCAAGAGTGAACCTGAAATCTATGTT 93
DB 504 CTACATCTACCATGCGCCAGAGGGGGTCCATCAGAAAGAGTCAAGTCTATGATG 563
OY 94 AGAAATRGAAAGTCTAGGCTGTTCTTGAGCCACACAGCAGATATTGCTTGA 153
DB 564 GTACCAAGTAGTGTATGAGTGGCTTCAGAGGACCGTGTGAAAGAGAGTGACA 623
OY 154 AGCTAAGCA 162
DB 624 AATTAAACA 632

RESULT 4
US-10-953-349-11978/c
;; Sequence 11978, Application US/10953349
;; Publication No. US20060107345A1
;; GENERAL INFORMATION:
;; APPLICANT: ALEXANDROV, Nikolai et al.
;; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;; FILE REFERENCE: 2750-1579PUS2
;; CURRENT APPLICATION NUMBER: US/10/953,349
;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: Patentin version 3.3
;; SEQ ID NO 11978

;; LENGTH: 393
;; TYPE: DNA
;; ORGANISM: Glycine max
US-10-953-349-11978

Query Match 13.8%; Score 27.6; DB 6; Length 393;
Best Local Similarity 52.8%; Pred. No. 1.3;
Matches 57; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

OY 26 CTGAGGCTTCATTCCTACAGAGTCAATCCGCGTGCACACCAAGAGTGAACCTGAATC 85
DB 144 CACAGAAATTAATCTTCTATGATGATGATGATGATGATGATGATGATGATGATG 85
OY 86 TCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCCACACA 133
DB 84 TCATGATCATGAAAGTAAAGTGAAGTCAAGACTCTACTAACAACAGAAC 37

RESULT 5
US-10-953-349-19516/c
;; Sequence 19516, Application US/10953349
;; Publication No. US20060107345A1
;; GENERAL INFORMATION:
;; APPLICANT: ALEXANDROV, Nikolai et al.
;; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;; FILE REFERENCE: 2750-1579PUS2
;; CURRENT APPLICATION NUMBER: US/10/953,349
;; CURRENT FILING DATE: 2004-09-30
;; NUMBER OF SEQ ID NOS: 40252
;; SOFTWARE: Patentin version 3.3
;; SEQ ID NO 19516
;; LENGTH: 1057
;; TYPE: DNA
;; ORGANISM: Glycine max
US-10-953-349-19516

Query Match 13.8%; Score 27.6; DB 6; Length 1057;
Best Local Similarity 52.8%; Pred. No. 1.9;
Matches 57; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

OY 26 CTGAGGCTTCATTCCTACAGAGTCAATCCGCGTGCACACCAAGAGTGAACCTGAATC 85
DB 799 CACAGAAATTAATCTTCTATGATGATGATGATGATGATGATGATGATGATGATG 740
OY 86 TCATGTTCAAGAAATGAAAGTGTCTAGGCTGTTCTTGAGCCACACA 133
DB 739 TCATGATCATGAAAGTAAAGTGAAGTCAAGACTCTACTAACAACAGAAC 692

RESULT 6
US-10-506-549-3/c
;; Sequence 3, Application US/10506549
;; Publication No. US20060100417A1
;; GENERAL INFORMATION:
;; APPLICANT: APPLERA CORPORATION
;; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;; FILE REFERENCE: C1001361-US
;; CURRENT APPLICATION NUMBER: US/10/506,549
;; CURRENT FILING DATE: 2004-09-03
;; PRIOR APPLICATION NUMBER: 60/361,343
;; PRIOR FILING DATE: 2002-03-05
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 394191
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(394191)

OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match 13.3%; Score 26.6; DB 6; Length 394191;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 28 CAAGGCTTCTCTACAGGTCATCCGGGTCACCAAGAGTGA 76
DB 4279 CAGAGCTTCTTACAGATCTTGGCTGCGAGATGAGAAAGGAA 4231

RESULT 7

US-10-953-349-15193
Sequence 15193, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15193
LENGTH: 1068
TYPE: DNA
ORGANISM: Glycine max
US-10-953-349-15193

Query Match 13.2%; Score 26.4; DB 6; Length 1068;
Best Local Similarity 47.0%; Pred. No. 5; Indels 0; Gaps 0;
Matches 78; Conservative 1; Mismatches 87; Indels 0; Gaps 0;

QY 10 TCATCTTTTCTAGGCTCTCAAGGCTTCTCATCTCAAGGTCATCTCTGGTGACACCAAG 69
DB 186 TTAATGCTCTGAGCTTCTCAAGGACACTGGCGGAGAGTGTGCTGCTCTCA 245
QY 70 AAGTGAACCTCGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTTTGGAGCCCA 129
DB 246 CGGTAGACACAACAATATGCGGATGACAGAGTGTGTTCAGGCGTTTCAGAGAGGTGA 305
QY 130 CACACAGATATTTGCTTGAAGCTAAGCAGGTAAGTCTGCTC 175
DB 306 AGAAGCCGATCTGCGCATTCATCAATCAATCAATGCTTCTCTCC 351

RESULT 8

US-10-953-349-9738
Sequence 9738, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9738
LENGTH: 3420
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-9738

Query Match 13.2%; Score 26.4; DB 6; Length 3420;
Best Local Similarity 54.3%; Pred. No. 8; Indels 0; Gaps 0;
Matches 51; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
QY 51 ATCTGGGTGACACCAAGAGTGAAGTCTGATCTGATGTTGAGAAATGAAAGTGTCT 110

DB 770 ATATGGGTTTCTCGAAGAAATCATGCCAGTATCAGTTTGAAGATGAAACTTGG 829

QY 111 AGCTGTTCTTGAGCCACACAGAGATATTTG 144
DB 830 TAGATGTTTTCAGCCACTTTTACGCCGAAGTTG 863

RESULT 9

US-10-511-937-2815/c
Sequence 2815, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Mohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2815
LENGTH: 6050
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-2815

Query Match 13.2%; Score 26.4; DB 6; Length 6050;
Best Local Similarity 50.0%; Pred. No. 11; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 TTGACATCTTCATCTTTTCTAGGCTCTCAAGGCTTCTTCTACAAGTCTATCTCGGCTG 60
DB 505 TTGCCATATGCAATTTGAGAGTGAATCTTCTGCTTCAAGTCTTCAAGTCTATCTTGGT 446
QY 61 CACACCAAGATGAACCTGGAATCTCATGTTTCAGAAATGAAAGTGTCTAGGCTGTCT 120
DB 445 AAGGTTCTGAGAAAGCTGGAGCTTCCATCTCCATCAATGATGATCATGATGACTGCAC 386
QY 121 TGAAGCCACAC 132
DB 385 TGAAGAAACCC 374

RESULT 10

US-11-293-697-1913/c
Sequence 1913, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1913
LENGTH: 3059
TYPE: DNA

ORGANISM: Homo sapiens
US-11-293-697-1913

Query Match 13.1%; Score 26.2; DB 7; Length 3059;
Best Local Similarity 51.3%; Pred. No. 9.3;
Matches 58; Conservative 1; Mismatches 54; Indels 0; Gaps 0;

QY 15 TTTTCTAGCTCCTCAAGGCTTTCATCCATCAAGTCACTCGGCGACACCAAGAGT 74
DB 2902 TTTTCTAGCTCCTCAAGGCTTTCATCCATCAAGTCACTCGGCGACACCAAGAGT 2843
QY 75 AACCTGATCTCATGTTTCAGAAATGAAATGTTAGCTGTTCTTGGAGCC 127
DB 2842 GGCCGCTCTCTCCGATCTGTAATAGTCTATGTTGTTCTTCTGGCC 2790

RESULT 11
US-11-217-529-79011

Sequence 79011, Application US/11217529
Publication No. US20060099612A1

GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 79011
LENGTH: 1008
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-79011

Query Match 12.7%; Score 25.4; DB 7; Length 1008;
Best Local Similarity 53.5%; Pred. No. 11;
Matches 53; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 56 GGGTGCACACCAAGAGTGAATCTGATCTCATGTTTCAAGAAATGAAATGTTGCT 115
DB 75 GGATGCGAGAAACGAGTGGAAATGCGAAATAATTCAAAAGAGCTTCAATATTTTC 134
QY 116 GTTCTGGAGCCCAACAGAGAGATATGCTTGTGCTAA 154
DB 135 GTCAATTAGACGACAGAGAGACAAATTTGACTGTGATA 173

RESULT 12
US-11-217-529-76402/C

Sequence 76402, Application US/11217529
Publication No. US20060099612A1

GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3

SEQ ID NO 76402
LENGTH: 1734
TYPE: DNA

ORGANISM: Saccharomyces pastorianus
US-11-217-529-76402

Query Match 12.6%; Score 25.2; DB 7; Length 1734;
Best Local Similarity 53.1%; Pred. No. 16;
Matches 51; Conservative 1; Mismatches 44; Indels 0; Gaps 0;

QY 65 CCAAGAGTGAACCTGCAATCTCATGTTTCAAGAAATGAAATGTTAGGCTTCTTGA 124
DB 940 CCAATCTGTAAGCTTCTTATGCTTCTTCAAGATCATACGTTCAATCTTCTTGG 881
QY 125 GCCCAGACAGCAGATATGCTTCTTCAAGCTAAG 160
DB 880 CACGACCAAGTATACCTTCTTCAATTTAGTTGAG 845

RESULT 13
US-11-293-697-740/C

Sequence 740, Application US/11293697
Publication No. US20060105376A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 740
LENGTH: 2638
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-740

Query Match 12.6%; Score 25.2; DB 7; Length 2638;
Best Local Similarity 54.3%; Pred. No. 19;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 7 TCCATCTTTTCAAGTCTCAAGGCTTTCATCAAGTCAATCTGCTGCTGACAGACC 66
DB 1751 TCCCTTCTGCTGCTTCTTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1692
QY 67 AAGAAGTGAACCTGAAATCTCATGTTTCAAGAAAT 100
DB 1691 GATCAGTGAATCTGCTGCTTCAATACCAAGGAGT 1658

RESULT 14
US-10-488-619-2493/C

Sequence 2493, Application US/10488619
Publication No. US20060099578A1

GENERAL INFORMATION:
APPLICANT: Greenlee, Winner and Sullivan, P.C.
TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Association
FILE REFERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2493
LENGTH: 631
TYPE: DNA
ORGANISM: Mus musculus
US-10-488-619-2493

Query Match 12.5%; Score 25; DB 6; Length 631;
Best Local Similarity 50.4%; Pred. No. 12;

Matches 58; Conservative 1; Mismatches 56; Indels 0; Gaps 0;

QY 81 GAATTCATGTTACAGAAATRGAAATGCTAGGCTGTTCTTGAGCCCAACAGACAGAT 140

DB 321 GGAGCTGAGTCTGTGAAAGCTGTACAGACTGTTCTCTAGCCCTAACGACGACG 262

QY 141 ATTGCTTGCTAAAGCTAAGCAGTACTGCTCACCTGTGCTTTCACCCCAAGC 195

DB 261 CATGATGCTGAGACGACGAGTGGCTCTTCTCTCCGAGGAGCCCAAGC 207

RESULT 15

US-10-505-928-226

/ Sequence 226, Application US/10505928

/ Publication No. US2006008532A1

/ GENERAL INFORMATION:

/ APPLICANT: Ludwig Institute for Cancer Research et al.

/ TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

/ FILE REFERENCE: 28967/39178

/ CURRENT APPLICATION NUMBER: US/10/505,928

/ PRIOR FILING DATE: 2004-08-27

/ NUMBER OF SEQ ID NOS: 866

/ SOFTWARE: Patentin 3.2

/ SEQ ID NO: 226

/ LENGTH: 4908

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-505-928-226

Query Match 12.5%; Score 25; DB 6; Length 4908;

Best Local Similarity 59.7%; Pred. No. 29;

Matches 40; Conservative 1; Mismatches 26; Indels 0; Gaps 0;

QY 88 ATGTTACGAAATRGAAATGCTAGGCTGTTCTTGAGCCCAACAGATATTGCTT 147

DB 1079 ATCTAACTAAGTAAATCTCTCAGGATTTCTTGAGGGCGTACAAACATCTATAAT 1138

QY 148 TGCTAAA 154

DB 1139 TGCAACA 1145

Search completed: May 26, 2006, 14:28:53

Job time : 25 secs